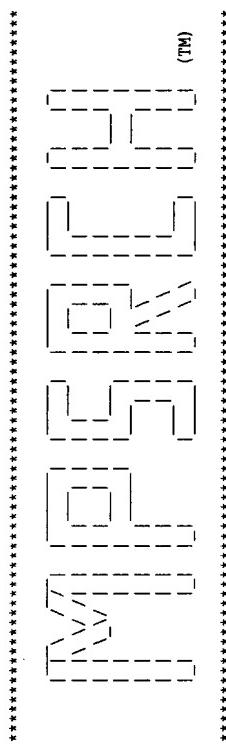


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/home/pandyamitterz/08_466_208P60535.rsp



Release 2.1D John F. Collins, Biocomputing Research Unit.
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MSearch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 21 12:18:25 1996; MasPar time 3.73 Seconds
591.501 Million cell updates/sec

Tabular output not generated.

Title: >p60535

Description: (1-144) from p60535.pep

Perfect Score: 100%

Sequence: 1 mklqllllgtvassisapx.....enlkdf1lxxpfdcwepvqx 144

Scoring table: PAM 150

Gap 11

Searched: 43470 seqs., 15335248 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot31
1:part2 2:part3 3:part4 5:part5 6:part6 7:part7
8:part8

Statistics: Mean 43.119; Variance 78.818; scale 0.547

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	Pred. No.
1	1002	99.4	144	2	CDF2 HUMAN	GRANULOCYTE-MACROPHAG	4.08e-194
2	828	82.1	144	2	CSF2 SHEEP	GRANULOCYTE-MACROPHAG	1.21e-154
3	773	76.7	143	2	CSF2 BOVIN	GRANULOCYTE-MACROPHAG	3.01e-147
4	536	53.2	141	2	CSF2 MOUSE	GRANULOCYTE-MACROPHAG	1.61e-89
5	102	10.1	605	1	BRL1 EBV	TRANSCRIPTION ACTIVAT	1.68e-02
6	100	9.9	581	4	MAYS YEAST	PROBABLE ALPHA-GLUCOS	3.25e-02
7	91	9.0	667	3	ENV GALV	ENV POLYPROTEIN PRECU	5.67e-01
8	90	8.9	567	1	ACHI DROME	ACETYLCHOLINE RECEPTO	7.69e-01
9	89	8.8	311	1	APE RAT	APOLIPOPROTEIN E PREC	1.04e+00
10	89	8.8	820	1	AK11 ECCLI	ASPAROKINASE I (EC 2	1.04e+00
11	88	8.7	133	1	SECR MOUSE	SECRETIN PRECURSOR	1.41e+00
12	88	8.7	200	2	CNTF RAT	CILIARY NEUROTROPHIC	1.41e+00
13	87	8.6	514	2	CPT7 ONCNY	CYTOCHROME P450 XVIIA	1.90e+00

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2

14	87	8.6	576	6	RPRP_BPSR	RNA-DIRECTED RNA POLY	1.90e+00
15	87	8.6	865	3	FLUG_EMENT	FLUG PROTEIN	1.90e+00
16	87	8.6	2201	1	ABC1_MOUSE	ATP-BINDING CASSETTE	1.90e+00
17	86	8.5	585	7	U132_YZVD	PROBABLE MAJOR ENVELO	2.51e+00
18	85	8.4	199	4	IL11_HUMAN	INTERLEUKIN-11 PRECUR	3.41e+00
19	85	8.4	403	2	CBGB3_CHICK	G2/MITOTIC-SPECIFIC C	3.41e+00
20	85	8.4	1407	6	PRO_DROME	PROTEIN PROSPERO	3.41e+00
21	84	8.3	304	8	YUJ2_CAEEL	HYPOTHETICAL 33.9 KD	4.51e+00
22	84	8.3	555	5	MIS_MOUSE	MUELLERIAN INHIBITING	4.51e+00
23	84	8.3	2429	7	SPCA_HUMAN	SPECTRIN ALPHA CHAIN	4.51e+00
24	83	8.2	311	1	APE_MOUSE	APOLIPOPROTEIN E PREC	6.07e+00
25	83	8.2	2505	3	FAS_RAT	FATTY ACID SYNTHASE	6.07e+00
26	82	8.1	184	7	TRIS_RABIT	TROPOBIN 1, SLOW SKEL	8.06e+00
27	82	8.1	199	4	IL11_MACFA	INTERLEUKIN-11 PRECUR	8.06e+00
28	82	8.1	200	6	PRIL2_OREMO	PROLACTIN II PRECURSO	8.06e+00
29	82	8.1	325	2	DBP_RAT	D-BINDING PROTEIN (DB	8.06e+00
30	82	8.1	597	7	V707_OYAV	66 KD PROTEIN	8.06e+00
31	81	8.0	313	5	OFLD_CANFA	OLFFACTORY RECEPTOR-LI	1.01e+01
32	81	8.0	385	3	ERBA_AVIER	ERBA ONCOGENE PROTEIN	1.01e+01
33	81	8.0	408	7	THA_CHICK	THYROID HORMONE RECP	1.01e+01
34	81	8.0	490	2	CPC6_RAT	CYTOCRHOME P450 IIC6	1.01e+01
35	81	8.0	705	2	CC5_YEAST	CELL CYCLE PROTEIN KI	1.01e+01
36	81	8.0	864	2	DYNMIN_1_HUMAN	DYNMIN-1.	1.07e+01
37	81	8.0	984	7	T3RE_SALTY	TYPE III RESTRICTION-	1.01e+01
38	81	8.0	1427	6	REST_HUMAN	RESTIN (CYTOSPLASMIC L	1.01e+01
39	81	8.0	3744	8	YIP9_YEAST	HYPOTHETICAL 433.2 KD	1.01e+01
40	80	7.9	186	7	TRIS_RAT	TROPOBIN 1, SLOW SKEL	1.41e+01
41	80	7.9	484	7	SCRB_VIBAL	SUCROSE-6-PHOSPHATE H	1.41e+01
42	80	7.9	851	2	DYN1_RAT	DYNMIN-1 (D100)	1.41e+01
43	80	7.9	861	2	DYNB_MOUSE	DYNMIN BREDDIN19.	1.41e+01
44	80	7.9	971	4	MCM3_YEAST	MINICHROMOSOME MAINT	1.41e+01
45	80	7.9	3054	6	POLG_TEV	GENOME POLYPROTEIN (C	1.41e+01

ALIGNMENTS

RESULT	1	HUMAN	STANDARD;	PRT;	144 AA.
ID	CSF2	HUMAN			
AC	P04141;				
DT	01-NOV-1986 (REL. 03, CREATED)				
DT	01-NOV-1986 (REL. 03, LAST SEQUENCE UPDATE)				
DT	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)				
DE	GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (GM-CSF)				
DE	(COLONY-STIMULATING FACTOR) (CSF).				
GN	CSF2 OR GMCSF.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUHTERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RM	85242684				
RA	LEE F., YOKOTA T., OTSURA T., GEMMELL L., LARSON N., LOH J.,				
RA	ARAI K.-I., RENNICK D.,				
RL	PROC. NATL. ACAD. SCI. U.S.A. 82:4360-4364 (1985).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RM	86205844				
RA	KAUSHANSKY K., O'HARA P.J., BERNICK K., SEGAL G.M., HAGEN F.S.,				
RA	ADAMSON J.W.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 83:3101-3105 (1986).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RM	85298329				
RA	CANTRELL M.A., ANDERSON D., CERRETTI D.P., PRICE V., MCKEREGHAN K.,				

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RA TUSHINSKI R.J., MOCHIZUKI D.Y., LARSEN A., GRABSTEIN K., COSMAN D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 82:6250-6254 (1985).
 RN [4]
 RP SEQUENCE FROM N.A.
 RM 85218749
 RA WONG G.G., WITEK J.S., TEMPLE P.A., WILKENS K.M., LEARY A.C.,
 LUXENBERG D.P., JONES S.S., BROWN E.L., KAY R.M., ORR E.C.,
 RA SHOEMAKER C., GOLDE D.W., KAUFMAN R.J., HEWICK R.M., WANG E.A.,
 CLARK S.C.;
 RL SCIENCE 228:810-815 (1985).
 RN [5]
 RP SEQUENCE FROM N.A.
 RM 86030234
 RA MIYATAKE S., OTSUKA T., YOKOTA T., LEE F., ARAI K.-I.;
 RL EMBO J. 4:2561-2568 (1985).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RM 92235840
 RA DIEDERICH K., BOONE T., KARPLUS P.A.;
 SCIENCE 254:1779-1782 (1991).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RM 92235844
 RA WALTER M.R., COOK W.J., EALICK S.E., NAGABHUSHAN T.L., TROTTA P.P.,
 BUGG C.E.;
 RL J. MOL. BIOL. 224:1075-1085 (1992).
 CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOEISIS BY CONTROLLING THE PRODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS, OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
 CC -!- FUNCTION: STIMULATES THE GROWTH AND DIFFERENTIATION OF HEMATOPOETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, INCLUDING CC GRANULOCYTES, MACROPHAGES, EOSINOPHILS AND ERYTHROCYTES.
 CC -!- SUBUNIT: MONOMER.
 DR EMBL; M13207; HSCSFMA.
 DR EMBL; M11734; HCCSFMB.
 DR EMBL; M11220; HSGMCSFA.
 DR EMBL; X03021; HGMCSFG.
 DR EMBL; M10663; HSCSFGM.
 DR PIR; A01853; FGHGM.
 DR PIR; C24636; C24636.
 DR PIR; A25169; A25169.
 DR PDB; 1CSG; 31-JUN-94.
 DR PDB; 1GMF; 31-OCT-93.
 DR PDB; 138950; 11TH EDITION.
 KW CYTOKINE; GROWTH FACTOR; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE;
 KW POLYMORPHISM.
 FT SIGNAL 1 17
 CHAIN 18 144
 FT DISULFID 1
 FT DISULFID 71 113
 FT DISULFID 105 138
 FT CARBOHYD 44 44
 FT CARBOHYD 54 54
 FT VARIANT 117 117
 FT TURN 25 27
 FT HELIX 30 44
 FT TURN 45 45
 FT HELIX 50 54
 FT STRAND 56 60
 FT HELIX 72 81
 FT TURN 82 82
 FT HELIX 85 103
 FT DISULFID 1
 FT DISULFID 105 138
 FT CARBOHYD 44 44
 FT SIGNAL 1 17
 FT CHAIN 18 144
 FT DISULFID 71 113
 FT DISULFID 105 138
 FT CARBOHYD 44 44
 SQ SEQUENCE 144 AA; 16295 MW; 112632 CN;
 FT TURN 104 104
 FT STRAND 115 119
 FT HELIX 120 131
 FT TURN 132 133
 SQ SEQUENCE 144 AA; 16295 MW; 112632 CN;

Query Match 99.4%; Score 1002; DB 2; Length 144;
 Best Local Similarity 95.1%; Pred. No. 4 08e-194;
 Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwqlslllgvacsisaparspsatgpwehnvaigearllnlrsdtaemnetvevi 60
 Qy 1 mwqlslllgvacisaparspsatgpwehnvaigearllnlrsdtaemnetvevi 60
 Db 61 semfdlqeqcigrlelykgqlrgslktkpltmashykhqcptpcatscatqxitf 120
 Qy 61 semfdlqeqcigrlelykgqlqsltkpltmashykhqcptpcatscatqxitf 120
 Db 121 esfkenlkdfllvipfdcwepvq 143
 Qy 121 esfkenlkdfllvipfdcwepvq 143
 PRT; 144 AA.

RESULT 2
 ID CSF2_SHEEP STANDARD
 AC P28773;
 DT 01-DEC-1992 (REL. 24, CREATED)
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
 DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
 DE GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (GM-CSF)
 DE (COLONY-STIMULATING FACTOR) (CSF).
 OS OVIS ARIES (SHEEP).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 9203044
 RA MCINNES C.J., HAIG M.C.K.;
 RL GENE 105:275-279 (1991).
 CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOEISIS BY CONTROLLING THE PRODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
 CC -!- FUNCTION: STIMULATES THE GROWTH AND DIFFERENTIATION OF HEMATOPOETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, INCLUDING CC GRANULOCYTES, MACROPHAGES, EOSINOPHILS AND ERYTHROCYTES.
 CC -!- SUBUNIT: MONOMER.
 DR EMBL; X53561; OGMCFSR.
 DR PIR; JH0469; JH0469.
 DR HSSP; P04141; ICSG.
 DR PROST; P500702; GM CSF.
 KW CYTOKINE; GROWTH FACTOR; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 17
 FT CHAIN 18 144
 FT DISULFID 71 113
 FT DISULFID 105 138
 FT CARBOHYD 44 44
 SQ SEQUENCE 144 AA; 16318 MW; 117795 CN;

Query Match 82.1%; Score 828; DB 2; Length 144;
 Best Local Similarity 77.6%; Pred. No. 1 21e-15;
 Matches 111; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

RA ALTMANN S.W., JOHNSON G.D., PRYSTONSKY M.B.;
 RL J. BIOL. CHEM. 266 5333-5341 (1991).
 CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
 CC CYTOKINES THAT ACT IN HEMATOPOIETIC CELLS BY CONTROLLING THE PRODUCTION,
 CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
 CC OF THE BLOOD. THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
 CC -!- FUNCTION: STIMULATES THE GROWTH AND DIFFERENTIATION OF
 CC HEMATOPOIETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, INCLUDING
 CC GRANULOCYTES, MACROPHAGES, EOSINOPHILS AND ERYTHROCYTES.
 CC -!- SUBUNIT: MONOMERIC.
 DR EMBL; X03020; NMIGMSFG.
 DR EMBL; X03019; NMIGMSFR.
 DR EMBL; M11847; NMCSGM.
 DR EMBL; X02333; NMIGMSFR.
 DR EMBL; X05906; NMIGMSFL.
 DR PIR; A01854; F0MSGM.
 DR PIR; A24644; A24644.
 DR PIR; A24645; A24645.
 DR PIR; A24636; A24635.
 DR HSSP; P04141; LCSC.
 DR PROSITE; PS00703; GM_CSF.
 KW CYTOKINE; GROWTH_FACTOR; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 17
 FT CHAIN 18 141
 FT DISULFID 68 110
 FT DISULFID 102 135
 FT CARBOHYD 83 83
 FT MUTAGEN 38 38
 FT MUTAGEN 73 73
 FT MUTAGEN 77 77
 FT MUTAGEN 80 80
 FT MUTAGEN 124 124
 FT CONFLICT 25 25
 FT CONFLICT 114 114
 FT CONFLICT 139 139
 FT CONFLICT 139 139
 SQ SEQUENCE 141 AA; 16090 MW; 112290 CN;
 Query Match 53.2%; Score 536; DB 2; Length 141;
 Best Local Similarity 52.4%; Pred. No. 1.61e-89;
 Matches 75; Conservative 20; Mismatches 45; Indels 3; Gaps 1;

Db 1 mwqlqllflglivwvslaptspitrspkveakhealhld--dmpvtlnneevv 57
 Qy 1 mwqlqlllgltvacisiaapxrspspsqwpewhnaqearrlhlndtaexnetvevk 60

Db 58 snefsfklltvcyqrlkfeeglrgntkkgalmatastyqtcptpetdetqvyt 117
 Qy 61 smrfdlqepctclqrlykqglsitkikgpltaashykhcpptpetscatqxitf 120

Db 118 adfidsktlfldpfleckpq 140
 Qy 121 estfknlkdflvvpfdoewpq 143

RESULT 6
 ID MAXS YEAST STANDARD; PRT; 581 AA.
 AC P40874;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE PROBABLE ALPHA-GLUCOSIDASE HRF581 (EC 3.2.1.20) (MALTASE).
 GN HRF581.
 OS SACCHAROMYCES CEREVIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA VANDENBOU M., DURAND P., BOLLE P.-A., DION C., PORTETELLE D.,
 RA HILGER F.;
 RL YEAST 10:1657-1662 (1994).
 CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING
 CC 1,4-LINKED D-GLUCOSE RESIDUES WITH RELEASE OF D-GLUCOSE.
 CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
 DR EMBL; Z334098; SCITEL.
 DR PIR; S45157; S45157.
 KW HYPOTHETICAL PROTEIN; HYDROLASE; GLYCOSIDASE; MALTOSE METABOLISM;
 KW MULTIGENE FAMILY.
 SQ SEQUENCE 581 AA; 67557 MW; 1153845 CN;

Query Match 9.9%; Score 100; DB 4; Length 581;
 Best Local Similarity 31.5%; Pred. No. 3.25e-02;
 Matches 17; Conservative 9; Mismatches 23; Indels 5; Gaps 4;

DB 290 gelnum-fnfk-htsvgenpkckyelipftlkdfklalaesflentdwstl 341
 DE TRANSCRIPTION ACTIVATOR BRIF1.

RESULT 5
 ID BRIF1 ERV STANDARD; PRT; 605 AA.
 AC P03205;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)

Qy 92 qpttumashyqkpcppptpscatqxitff--esfkenlkd-fllvwpfdcwepv 142
 AC P21415;
 DT 01-MAY-1991 (REL. 18, CREATED)
 DT 01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
 DT 01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)

DE ENV POLYPROTEIN PRECURSOR (CONTAINS: KNOB PROTEIN GP70; SPIKE PROTEIN P15E).
 GN ENV.
 OS GIBBON APE LEUKEMIA VIRUS.

OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
 OC ONCOVIRINAE.
 RN [1]

RM 90051069
 RP SEQUENCE FROM N.A.

RA DELASSUS S., SONIGO P., WAIN-HOBSON S.;
 RL VIRIOLOGY 175: 205-213 (1989).
 DR EMBL: M24921; PDB: C32395; PDB: C32395; VCLJG;.;

DR PIR: C32395; VCLJG;.;

KW COAT PROTEIN; GLYCOPROTEIN; POLYPROTEIN; TRANSMEMBRANE; SIGNAL.

FT CHAIN 1 42
 FT CHAIN 43 489
 FT CHAIN 490 667
 FT TRANSMEM 492 508
 FT TRANSMEM 637 653
 FT CARBOHYD 301 301
 FT CARBOHYD 344 344
 FT CARBOHYD 415 415
 FT CARBOHYD 421 421
 FT CARBOHYD 433 433
 FT CARBOHYD 453 453
 SQ SEQUENCE 667 AA; 737/29 MW; 2334159 CN;

FT CHAIN 22 567
 FT DOMAIN 22 240
 FT DOMAIN 241 264
 FT TRANSMEM 272 290
 FT TRANSMEM 306 325
 FT DOMAIN 326 513
 FT TRANSMEM 514 532
 FT DISULFID 149 163
 FT DISULFID 222 223
 FT TRANSMEM 272 290
 FT CARBOHYD 45 45
 FT CARBOHYD 233 233
 FT VARIANT 538 538
 SQ SEQUENCE 567 AA; 64016 MW; 1720346 CN;

FT DISULFID 149 163
 FT DISULFID 222 223
 FT TRANSMEM 272 290
 FT CARBOHYD 45 45
 FT CARBOHYD 233 233
 FT VARIANT 538 538
 SQ SEQUENCE 567 AA; 64016 MW; 1720346 CN;

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 FT DISULFID 222 223
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 FT TRANSMEM 272 290
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 FT CARBOHYD 233 233
 FT VARIANT 538 538
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 FT CARBOHYD 233 233
 FT VARIANT 538 538
 SQ SEQUENCE 567 AA; 64016 MW; 1720346 CN;

FT DISULFID 149 163
 FT DISULFID 222 223
 FT TRANSMEM 272 290
 FT CARBOHYD 45 45
 FT CARBOHYD 233 233
 FT VARIANT 538 538
 SQ SEQUENCE 567 AA; 64016 MW; 1720346 CN;

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 FT TRANSMEM 272 290
 FT CARBOHYD 45 45
 FT CARBOHYD 233 233
 FT VARIANT 538 538
 SQ SEQUENCE 567 AA; 64016 MW; 1720346 CN;

CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- TISSUE SPECIFICITY: CNS IN EMBRYOS.
 CC -!- DEVELOPMENTAL STAGE: LATE EMBRYONIC, LATE PUPAL AND SECOND INSTAR
 CC LARVAE STAGES.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
 DR EMBL: X07194; DMLSR.
 DR PIR: S00381; ACFFAI.
 DR FLYBASE: FRGN00034; ACR96AA.
 DR PROSITE; PS00236; NEUROTR. ION CHANNEL.
 KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
 KW TRANSMEMBRANE; MULTIGENE FAMILY.

FT CHAIN 22 567
 FT DOMAIN 22 240
 FT DOMAIN 241 264
 FT TRANSMEM 272 290
 FT TRANSMEM 306 325
 FT DOMAIN 326 513
 FT DOMAIN 327 532
 FT TRANSMEM 348 552
 FT TRANSMEM 351 572
 FT TRANSMEM 354 592
 FT TRANSMEM 357 612
 FT TRANSMEM 360 632
 FT TRANSMEM 363 652
 FT TRANSMEM 366 672
 FT TRANSMEM 369 692
 FT TRANSMEM 372 712
 FT TRANSMEM 375 732
 FT TRANSMEM 378 752
 FT TRANSMEM 381 772
 FT TRANSMEM 384 792
 FT TRANSMEM 387 812
 FT TRANSMEM 390 832
 FT TRANSMEM 393 852
 FT TRANSMEM 396 872
 FT TRANSMEM 399 892
 FT TRANSMEM 402 912
 FT TRANSMEM 405 932
 FT TRANSMEM 408 952
 FT TRANSMEM 411 972
 FT TRANSMEM 414 992
 FT TRANSMEM 417 1012
 FT TRANSMEM 420 1032
 FT TRANSMEM 423 1052
 FT TRANSMEM 426 1072
 FT TRANSMEM 429 1092
 FT TRANSMEM 432 1112
 FT TRANSMEM 435 1132
 FT TRANSMEM 438 1152
 FT TRANSMEM 441 1172
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 FT TRANSMEM 447 1212
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 FT TRANSMEM 453 1252
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 FT TRANSMEM 480 1432
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 FT TRANSMEM 531 1772
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 FT TRANSMEM 537 1812
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 FT TRANSMEM 543 1852
 FT TRANSMEM 546 1872
 FT TRANSMEM 549 1892
 FT TRANSMEM 552 1912
 FT TRANSMEM 555 1932
 FT TRANSMEM 558 1952
 FT TRANSMEM 561 1972
 FT TRANSMEM 564 1992
 FT TRANSMEM 567 2012
 FT TRANSMEM 570 2032
 FT TRANSMEM 573 2052
 FT TRANSMEM 576 2072
 FT TRANSMEM 579 2092
 FT TRANSMEM 582 2112
 FT TRANSMEM 585 2132
 FT TRANSMEM 588 2152
 FT TRANSMEM 591 2172
 FT TRANSMEM 594 2192
 FT TRANSMEM 597 2212
 FT TRANSMEM 600 2232
 FT TRANSMEM 603 2252
 FT TRANSMEM 606 2272
 FT TRANSMEM 609 2292
 FT TRANSMEM 612 2312
 FT TRANSMEM 615 2332
 FT TRANSMEM 618 2352
 FT TRANSMEM 621 2372
 FT TRANSMEM 624 2392
 FT TRANSMEM 627 2412
 FT TRANSMEM 630 2432
 FT TRANSMEM 633 2452
 FT TRANSMEM 636 2472
 FT TRANSMEM 639 2492
 FT TRANSMEM 642 2512
 FT TRANSMEM 645 2532
 FT TRANSMEM 648 2552
 FT TRANSMEM 651 2572
 FT TRANSMEM 654 2592
 FT TRANSMEM 657 2612
 FT TRANSMEM 660 2632
 FT TRANSMEM 663 2652
 FT TRANSMEM 666 2672
 FT TRANSMEM 669 2692
 FT TRANSMEM 672 2712
 FT TRANSMEM 675 2732
 FT TRANSMEM 678 2752
 FT TRANSMEM 681 2772
 FT TRANSMEM 684 2792
 FT TRANSMEM 687 2812
 FT TRANSMEM 690 2832
 FT TRANSMEM 693 2852
 FT TRANSMEM 696 2872
 FT TRANSMEM 699 2892
 FT TRANSMEM 702 2912
 FT TRANSMEM 705 2932
 FT TRANSMEM 708 2952
 FT TRANSMEM 711 2972
 FT TRANSMEM 714 2992
 FT TRANSMEM 717 3012
 FT TRANSMEM 720 3032
 FT TRANSMEM 723 3052
 FT TRANSMEM 726 3072
 FT TRANSMEM 729 3092
 FT TRANSMEM 732 3112
 FT TRANSMEM 735 3132
 FT TRANSMEM 738 3152
 FT TRANSMEM 741 3172
 FT TRANSMEM 744 3192
 FT TRANSMEM 747 3212
 FT TRANSMEM 750 3232
 FT TRANSMEM 753 3252
 FT TRANSMEM 756 3272
 FT TRANSMEM 759 3292
 FT TRANSMEM 762 3312
 FT TRANSMEM 765 3332
 FT TRANSMEM 768 3352
 FT TRANSMEM 771 3372
 FT TRANSMEM 774 3392
 FT TRANSMEM 777 3412
 FT TRANSMEM 780 3432
 FT TRANSMEM 783 3452
 FT TRANSMEM 786 3472
 FT TRANSMEM 789 3492
 FT TRANSMEM 792 3512
 FT TRANSMEM 795 3532
 FT TRANSMEM 798 3552
 FT TRANSMEM 801 3572
 FT TRANSMEM 804 3592
 FT TRANSMEM 807 3612
 FT TRANSMEM 810 3632
 FT TRANSMEM 813 3652
 FT TRANSMEM 816 3672
 FT TRANSMEM 819 3692
 FT TRANSMEM 822 3712
 FT TRANSMEM 825 3732
 FT TRANSMEM 828 3752
 FT TRANSMEM 831 3772
 FT TRANSMEM 834 3792
 FT TRANSMEM 837 3812
 FT TRANSMEM 840 3832
 FT TRANSMEM 843 3852
 FT TRANSMEM 846 3872
 FT TRANSMEM 849 3892
 FT TRANSMEM 852 3912
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 FT TRANSMEM 858 3952
 FT TRANSMEM 861 3972
 FT TRANSMEM 864 3992
 FT TRANSMEM 867 4012
 FT TRANSMEM 870 4032
 FT TRANSMEM 873 4052
 FT TRANSMEM 876 4072
 FT TRANSMEM 879 4092
 FT TRANSMEM 882 4112
 FT TRANSMEM 885 4132
 FT TRANSMEM 888 4152
 FT TRANSMEM 891 4172
 FT TRANSMEM 894 4192
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 FT TRANSMEM 918 4352
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 FT TRANSMEM 939 4492
 FT TRANSMEM 942 4512
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 FT TRANSMEM 957 4612
 FT TRANSMEM 960 4632
 FT TRANSMEM 963 4652
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 FT TRANSMEM 969 4692
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 FT TRANSMEM 978 4752
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 FT TRANSMEM 984 4792
 FT TRANSMEM 987 4812
 FT TRANSMEM 990 4832
 FT TRANSMEM 993 4852
 FT TRANSMEM 996 4872
 FT TRANSMEM 999 4892
 FT TRANSMEM 1002 4912
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 FT TRANSMEM 1101 5572
 FT TRANSMEM 1104 559

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RA	MCLEAN J.W., FUKAZAWA C., TAYLOR J.M.;	OC	ENTEROBACTERIACEAE.
RL	J. BIOL. CHEM. 258:8913-9000(1983).	[1]	SEQUENCE FROM N.A.
CC	-!- FUNCTION: APO-E MEDIATES BINDING, INTERNALIZATION, AND CATABOLISM OF LIPOPROTEIN PARTICLES IT CAN SERVE AS A LIGAND FOR THE LDL(APO B/E) RECEPTOR AND FOR THE SPECIFIC APO-E RECEPTOR (CHYLOMICRON REMNANT) OF HEPATIC TISSUES.	RP	SEQUENCE FROM N.A.
CC	-!- SUBCELLULAR LOCATION: EXTRACELLULAR.	RM	81077247
CC	-!- THE MATURE PROTEIN HAS NO CYSTEINE RESIDUES; HOWEVER, IN DIFFERENT ALLELIC VARIANTS WHERE CYSTEINE RESIDUES REPLACE ARGinine AT POSITIONS 115 OR 168, BINDING OF APO-E TO CELL MEMBRANE RECEPTORS IS DECREASED. THE AMINO END OF THIS PROTEIN IS THEREFORE THOUGHT TO INTERACT WITH THE RECEPTOR.	RA	KATINKA M., COSSART P., SIBILLI L., SAINT-GIRONS I., CHALVIGNAC M.A., LE BRAS G., COHEN G.N., YANTV M.;
CC	ISBML; X04979; RNAOEG.	RA	ISONO K., MIZOBUCHI K., NAKATA A.;
-DR	EMBL; J07582; RNAP0EA.	RA	YURA T., MORI H., NAGAI H., NAGATA T., ISHIHAMA A., FUJITA N.,
CC	DR	RA	[2]
CC	PIR; A03094; LERTE.	RN	NUCLEIC ACIDS RES. 20:3305-3308(1992).
CC	DR	RN	[3]
CC	PIR; A25576; A25576.	RP	SEQUENCE FROM N.A.
CC	DR	RC	STRAIN-K12;
CC	PIR; A26189; A26189.	RM	92334977
DR	HSSP; P02649; 11E4.	RA	STRAIN-K12 / MG1655;
DR	GLYCOPROTEIN; PLASMA; LIPID TRANSPORT; HDL; VLDL; CHYLOMICRON; STATIC ACID; HEPARIN-BINDING; REPET; SIGNAL.	RA	BURLAND V.D., PLUNKETT G. III, BLATTNER F.R.;
KW	SIGNAL	RL	SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDJB DATA BANKS.
FT	CHAIN	RA	[4]
FT	19	RM	SEQUENCE OF 51-129.
FT	311	RM	80043179
FT	HEPARIN-BINDING (BY SIMILARITY).	RA	SIBILLI L., LE BRAS G., COSSART P., CHALVIGNAC M.A., LE BRAS G.,
FT	DOMAIN	RA	BRILEY P.A., COHEN G.N.;
FT	154	RA	BIOCHIMIE 61:733-739(1979).
FT	157	RA	[5]
FT	220	RM	REVISION TO 11.
FT	227	RA	83135751
FT	246	RA	COSSET P.;
FT	DOMAIN	RL	UNPUBLISHED RESULTS, CITED BY:
FT	72	RL	ZAKIN M.M., DUCHANGE N., FERRARA P., COHEN G.N.;
FT	93	RL	J. BIOL. CHEM. 258:3028-3031(1983).
FT	REPEAT	CC	-!- PATHWAY: CATALYZES 2 NONCONSECUTIVE REACTIONS IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE AND LYS.
FT	94	CC	TO MET, AND TO THR AND ILE.
FT	115	CC	-!- CATALYTIC ACTIVITY: L-HOMOCYSTEINE + NAD(P)(+) = L-ASPARTATE
FT	137	CC	BETA-SEMITAIDENYL + NAD(P)H.
FT	138	CC	-!- CATALYTIC ACTIVITY: ATP + LASPARTATE = ADP + 4-PHOSPHO-L-
FT	159	CC	ASPARTATE.
FT	181	CC	-!- SUBUNIT: HOMOTRIMER.
FT	182	CC	-!- ENZYME REGULATION: THE ENZYME ACTIVITIES ARE REGULATED ALLOSTERICALLY BY L-THREONINE.
FT	204	CC	-!- ASPARTOKINASE II-HOMOSERINE DEHYDROGENASE II AND ASPARTOKINASE III ALSO CATALYZE THE SAME REACTION(S).
FT	224	CC	-!- SIMILARITY: TO OTHER ASPARTOKINASES AND HOMOSERINE DEHYDROGENASES.
FT	246	DR	EMBL; W00361; ECFRA.
FT	8	DR	EMBL; J001706; ECFHR.
FT	8	DR	EMBL; X68872; ECFHRR.
FT	8	DR	EMBL; D10483; ECAPAO2.
FT	8	DR	EMBL; U14003; ECW93.
FT	Qy	DR	PIR; A00671; DECK.
FT	56	DR	PIR; S40531; S40531.
FT	56	DR	ECOGENE; EG10398; TTRA.
FT	56	DR	PROSITE; PS00324; ASPARTOKINASE.
FT	Db	KW	TRANSFERASE; KINASE; OXIDOREDUCTASE; THREONINE BIOSYNTHESIS; NADP; ALLOSTERIC ENZYME; MULTIFUNCTIONAL ENZYME.
FT	4	FT	DOMAIN
FT	4	FT	1
FT	4	FT	249
FT	4	FT	ASPARTOKINASE I.
FT	21-JUL-1986 (REL. 01, CREATED)	FT	DOMAIN
FT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)	FT	250
FT	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)	FT	470
FT	ASPARTOKINASE I (EC 2.7.2.4) / HOMOSERINE DEHYDROGENASE I (EC 1.1.1.3)	FT	470
FT	DE	FT	INTERFACE.
FT	TTRA (TTHRA1; TTHRA2).	FT	HOMOSERINE DEHYDROGENASE I.

RESULT 11
 ID SECR_MOUSE STANDARD; PRT; 133 AA.
 AC Q08535;
 DT 01-OCT-1994 (REL. 30, CREATED)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE SECRETIN PRECURSOR,
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 9473495
 RA LAN M.S., KAJIYAMA W., DONADEL G., LU J., NOTKINS A.L.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 200:1066-1071 (1994).
 CC -!- FUNCTION: STIMULATES FORMATION OF NAHCO (3)-RICH PANCREATIC JUICE
 AND SECRETION OF NAHCO (3)-RICH BILE AND INHIBITS HCL PRODUCTION
 BY THE STOMACH.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR EMBL; X73580; MMSECR.
 DR PIR; JC2202; JC2207.
 DR PIR; S34214; S34214.
 KW GLUCAGON FAMILY; HORMONE; AMIDATION; SIGNAL.
 FT SIGNAL 1 22 BY SIMILARITY.
 FT PEPTIDE 32 58 SECRETIN (BY SIMILARITY).
 FT MOD RES 58 58 AMIDATION (G-59 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 133 AA; 14914 MW; 92729 CN;

Query Match 8.7%; Score 88; DB 7; Length 133;
 Best Local Similarity 28.2%; Pred. No. 1.41e+00;
 Matches 22; Conservative 18; Mismatches 34; Indels 4; Gaps 4;

Db 9 mllllllllsssa-alpappptphsgmftselqlsarlqlqllgvlgrseqdte 67
 Qy 1 mwllllllllqvacisapxrspsxcpw-ehvnaiqearllnlsrdtaexne-tve 58

Db 68 nipep-slarksplkpledq 84
 Qy 59 vxsemfdiqeqptclqtrt 76

RESULT 12
 ID CNTR_RAT STANDARD; PRT; 200 AA.
 AC P20294;
 DT 01-FEB-1991 (REL. 17, CREATED)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)

DE CILIARY NEUROTROPHIC FACTOR (CNTRF).
 FT CONFICT 375 375 L -> Q (IN REF. 3).
 FT CONFICT 393 393 A -> T (IN REF. 3).
 FT CONFICT 406 406 L -> M (IN REF. 3).
 FT CONFICT 553 553 N -> D (IN REF. 3).
 FT CONFICT 607 607 I -> T (IN REF. 3).
 FT CONFICT 658 658 R -> T (IN REF. 3).
 SQ SEQUENCE 820 AA; 89122 MW; 3251159 CN;

Query Match 8.8%; Score 89; DB 1; Length 820;
 Best Local Similarity 27.0%; Pred. No. 1.04e+00;
 Matches 10; Conservative 17; Mismatches 9; Indels 1; Gaps 1;

. Db 669 dprddlgmavarkllilarctgreladieptevl 705
 * Qy 28 qp*ehvnaiqearllnlsrdtaexn-etvxxsem 63

RESULT 11
 ID SECR_MOUSE STANDARD; PRT; 133 AA.
 AC P30437;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE CYTOCHROME P450 XVIIA1 (P450-C17) (EC 1.14.99.9) (STEROID 17-ALPHA-HYDROXYLASE/11,20 LYASE).
 DR PIR; S34214; S34214.
 KW ONCORHYNCHUS MYKISS (RAINBOW TROUT) (SALMO GARDNERI).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
 OC OSTEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 93083625
 RA SAKAI N., TANAKA M., ADACHI S., MILLER W.L., NAGAHAMA Y.;
 RL FEBS LETT. 301:60-64 (1992).
 CC -!- FUNCTION: CONVERSION OF PREGNENOLONE AND PROGESTERONE TO THEIR
 17-ALPHA-HYDROXYLATED PRODUCTS AND SUBSEQUENTLY TO
 DEHYDROEPITANOSTERONE (DHEA) AND ANDROSTENEDIONE. CATALYZES
 BOTH THE 17-ALPHA-HYDROXYLATION AND THE 17,20-LYASE REACTION.
 CC -!- CATALYTIC ACTIVITY + AH(2) + OH(2) = A 17-ALPHA-HYDROXYSTEROID + A + H(2)O.
 CC -!- PATHWAY: KEY ENZYME IN STEROIDGENIC PATHWAY.
 CC -!- SIMILARITY: MEMBER OF THE CYTOCHROME P-450 FAMILY.
 DR EMBL; X53800; SGCP1R.
 DR PIR; S21125; S21125.

Query Match 8.7%; Score 88; DB 7; Length 133;
 Best Local Similarity 28.2%; Pred. No. 1.41e+00;
 Matches 22; Conservative 18; Mismatches 34; Indels 4; Gaps 4;

Db 9 mllllllllsssa-alpappptphsgmftselqlsarlqlqllgvlgrseqdte 67
 Qy 1 mwllllllllqvacisapxrspsxcpw-ehvnaiqearllnlsrdtaexne-tve 58

Db 68 nipep-slarksplkpledq 84
 Qy 59 vxsemfdiqeqptclqtrt 76

RESULT 12
 ID CNTR_RAT STANDARD; PRT; 200 AA.
 AC P20294;
 DT 01-FEB-1991 (REL. 17, CREATED)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)

DE RATTUS NORVEGICUS (RAT).
 FT CONFICT 553 553 EURKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 FT CONFICT 607 607 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RM 90081871
 RA STOCKLI K.A., LOTTSPICHL F., SENDTNER M., MASTAKOWSKI P., CARROLL P.,
 RA GOETZ R., LINDBOM D., THOENEN H.;
 RL NATURE 342:920-923 (1989).
 CC -!- FUNCTION: CNTRF IS A SURVIVAL FACTOR FOR VARIOUS NEURONAL CELL
 TYPES. SEEKS TO PREVENT THE DEGENERATION OF MOTOR AXONS AFTER
 AXOTOMY.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- TISSUE SPECIFICITY: NERVOUS SYSTEM.
 CC -!- SIMILARITY: HIGH, WITH OTHER MAMMALIAN CNTRF.
 DR EMBL; X17457; RNCNTF.
 DR PIR; S08144; UNRCNTF.
 KW GROWTH FACTOR/ NEURONE.
 SQ SEQUENCE 200 AA; 22854 MW; 206472 CN;

Query Match 8.7%; Score 88; DB 2; Length 200;
 Best Local Similarity 31.3%; Pred. No. 1.41e+00;
 Matches 15; Conservative 12; Mismatches 18; Indels 3; Gaps 3;

Db 44 Inknnildsvdqvavastdrwsmttearilgenldqayr-tfcgmltk1 90
 Qy 45 lsrdataaexnetverxs-emf-dldeptcdlrlqlycqqlqsltk1 90

RESULT 13
 ID ONCMTY STANDARD; PRT; 514 AA.
 AC P30437;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE CYTOCHROME P450 XVIIA1 (P450-C17) (EC 1.14.99.9) (STEROID 17-ALPHA-HYDROXYLASE/11,20 LYASE).
 DR PIR; S34214; S34214.
 KW ONCORHYNCHUS MYKISS (RAINBOW TROUT) (SALMO GARDNERI).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
 OC OSTEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 93083625
 RA SAKAI N., TANAKA M., ADACHI S., MILLER W.L., NAGAHAMA Y.;
 RL FEBS LETT. 301:60-64 (1992).
 CC -!- FUNCTION: CONVERSION OF PREGNENOLONE AND PROGESTERONE TO THEIR
 17-ALPHA-HYDROXYLATED PRODUCTS AND SUBSEQUENTLY TO
 DEHYDROEPITANOSTERONE (DHEA) AND ANDROSTENEDIONE. CATALYZES
 BOTH THE 17-ALPHA-HYDROXYLATION AND THE 17,20-LYASE REACTION.
 CC -!- CATALYTIC ACTIVITY + AH(2) + OH(2) = A 17-ALPHA-HYDROXYSTEROID + A + H(2)O.
 CC -!- PATHWAY: KEY ENZYME IN STEROIDGENIC PATHWAY.
 CC -!- SIMILARITY: MEMBER OF THE CYTOCHROME P-450 FAMILY.
 DR EMBL; X53800; SGCP1R.
 DR PIR; S21125; S21125.

Query Match 8.6%; Score 87; DB 2; Length 514;

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15

Best Local Similarity 35.1%; Pred. No. 1.90e+00;
 Matches 20; Conservative 11; Mismatches 24; Indels 2; Gaps 2;

Db 263 heqrldldallrakrsaaenntaeitmetvglsedhilmvtgdfifagettstvlik 319
 Qy 37 qearrlin-lsrdrt-aaexnetveyxsemfdqspclqrtrlekgqlagsltlk 91

RESULT 14

ID	RP01BPSP	STANDARD	PRT;	516 AA.
AC	P0975;			
DT	01-MAR-1989 (REL. 10, CREATED)			
•	01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)			
DT	01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)			
•	DE RNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.48) (RNA REPLICASE			
•	DE BETA CHAIN.			
OS	BACTERIOPHAGE SP.			
OC	VIRIDAE; SS-RNA NONENVELOPED VIRUSES; LEVIVIRIDAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RM	88289362			
RA	HIRASHIMA A., HIROSE T., INAYAMA S., INOKUCHI Y., JACOBSON A. B.;			
RL	NUCLEIC ACIDS RES. 16:6205-6221(1988).			
CC	-!- FUNCTION: THIS ENZYME IS PART OF THE VIRAL RNA-DEPENDENT RNA POLYMERASE COMPLEX.			
CC	-!- SUBUNIT: THE POLYMERASE COMPLEX IS COMPOSED OF FOUR CHAINS, THE THREE OTHER PROTEINS OF THE COMPLEX (ALPHA, GAMMA, AND DELTA CHAINS) ARE SUPPLIED BY THE HOST CELL.			
DR	EMBL; X07489; MYSPXX.			
DR	PIR; SU1965; S01965.			
KW	RNA-DIRECTED RNA POLYMERASE.			
SQ	SEQUENCE 516 AA; 65397 MW; 1707305 CN;			

Query Match 8.6%; Score 87; DB 6; Length 576;

Best Local Similarity 22.6%; Pred. No. 1.90e+00;
 Matches 12; Conservative 19; Mismatches 21; Indels 1; Gaps 1;

Db 199 rvnevrtsnkavtypknsktdrclaiapgwmmfffqlygvavirdrkrkl 251
 Qy 32 hynaiqearrlinlsrdtaexnetveyxsemfd-qspclqrtrleykqgl 83

RESULT 15

RP SEQUENCE FROM N.A.

RA LEE B., ADAMS T. H.;
 RL SUBMITTED (XXX-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
 CC -!- FUNCTION: REQUIRED FOR PRODUCTION OF AN EXTRACELLULAR DEVELOPMENTAL SIGNAL.
 CC -!- SIMILARITY: TO PROKARYOTIC GLUTAMINE SYNTHETASE I.
 DR EMBL; L27817; ENFLUG.

SEQUENCE 855 AA; 96305 MW; 3869940 CN;
 RP SEQUENCE FROM N.A.

RA LEE B., ADAMS T. H.;
 RL SUBMITTED (XXX-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
 CC -!- FUNCTION: REQUIRED FOR PRODUCTION OF AN EXTRACELLULAR DEVELOPMENTAL SIGNAL.
 CC -!- SIMILARITY: TO PROKARYOTIC GLUTAMINE SYNTHETASE I.
 DR EMBL; L27817; ENFLUG.

SEQUENCE 855 AA; 96305 MW; 3869940 CN;
 Query Match 8.6%; Score 87; DB 3; Length 865;
 Best Local Similarity 22.6%; Pred. No. 1.90e+00;

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16

Best Local Similarity 35.1%; Pred. No. 1.90e+00;
 Matches 20; Conservative 11; Mismatches 24; Indels 3; Gaps 3;

Db 263 iervflkpttdptgeedapsnthsqmt-t-retrmlplleia-eliasighlq 621
 Qy 3 lqsllllgvcasisapxrspssxpwehnaiqearrlinlsrdtaexnetveyxse 62

RESULT 14

ID	RP01BPSP	STANDARD	PRT;	516 AA.
AC	P0975;			
DT	01-MAR-1989 (REL. 10, CREATED)			
•	01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)			
DT	01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)			
•	DE RNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.48) (RNA REPLICASE			
•	DE BETA CHAIN.			
OS	BACTERIOPHAGE SP.			
OC	VIRIDAE; SS-RNA NONENVELOPED VIRUSES; LEVIVIRIDAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RM	88289362			
RA	HIRASHIMA A., HIROSE T., INAYAMA S., INOKUCHI Y., JACOBSON A. B.;			
RL	NUCLEIC ACIDS RES. 16:6205-6221(1988).			
CC	-!- FUNCTION: THIS ENZYME IS PART OF THE VIRAL RNA-DEPENDENT RNA POLYMERASE COMPLEX.			
CC	-!- SUBUNIT: THE POLYMERASE COMPLEX IS COMPOSED OF FOUR CHAINS, THE THREE OTHER PROTEINS OF THE COMPLEX (ALPHA, GAMMA, AND DELTA CHAINS) ARE SUPPLIED BY THE HOST CELL.			
DR	EMBL; X07489; MYSPXX.			
DR	PIR; SU1965; S01965.			
KW	RNA-DIRECTED RNA POLYMERASE.			
SQ	SEQUENCE 516 AA; 65397 MW; 1707305 CN;			

Search completed: Fri Jun 21 12:19:07 1996
 Job time : 42 secs.

[lin 2] [12] [0] [/home/pattayu/mesa-0.8.4/tst/3081P035108]

JHEP09(2011)029

(All)

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Search on mountain database enough within Smith Mountain

run on: Fri Jun 21 12:00:00 1996
tabular output not generated.

title: >P60535
description: (1-44) from p60535.pep
secondary_structures: 100%
score: 100

sequence: 1 mw1qsl1llgtvacisapx.....en1kdf1l1vxprdcwepvpx 144
scoring table: PAM 150

SABURŌ TAKAHASHI / SHIBAICHI

post-processing: Minimum Match

1:part1 2:part2 3:part3

Statistics: Mean 30.234; Variance 133.218; scale 0.227
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1008	100.0	144	2 P811886	Sequence of human gra	3.92e-84
2	1008	100.0	144	3 P60535	Colony stimulating fa	3.92e-84
3	1002	99.4	144	13 R71118	GM-CSF encoded by clo	1.48e-83
4	1002	99.4	144	3 P60418	Human granulocyte mac	1.48e-83
5	1002	99.4	144	2 P70657	Sequence of a human g	1.48e-83
6	1002	99.4	144	1 R04098	Metaproteasechase gen	1.48e-83
7	1002	99.4	144	2 P811885	Sequence of human gra	1.48e-83
8	993	98.5	144	1 P80527	Granulocyte macrophag	1.08e-82
9	993	98.5	144	2 P70656	Sequence of a human g	4.08e-82
10	976	96.8	142	2 P94855	Human granulocyte mac	4.63e-81
11	899	89.2	131	2 P70351	Sequence of granulocy	1.11e-73
12	895	88.8	131	3 P60350	Human granulocyte mac	2.69e-73

1m 21 12 10 /home/handval/metz 0.8 466 105/1200535 1.0

14	871	86.4	127	3	R13215	Oxidised GM-CSF.	5.33e-71
15	871	86.4	127	7	R33774	Recombinant human Granulocyte-macrophage colony-stimulating factor.	5.33e-71
16	871	86.4	128	1	P90118	Synthetic human granulocyte-macrophage colony-stimulating factor.	5.33e-71
17	871	86.4	128	1	P90115	Synthetic human granulocyte-macrophage colony-stimulating factor.	5.33e-71
18	864	85.7	127	14	R72357	Human granulocyte-macrophage colony-stimulating factor.	2.49e-70
19	864	85.7	127	1	P91061	Human granulocyte-macrophage colony-stimulating factor.	2.49e-70
20	864	85.7	127	1	P91899	Amino acid sequence of human granulocyte-macrophage colony-stimulating factor.	2.49e-70
21	862	85.5	128	1	R03199	New human granular macrophage colony-stimulating factor.	3.87e-70
22	861	85.4	128	1	P81001	Sequence (I) of human granulocyte-macrophage colony-stimulating factor.	4.82e-70
23	860	85.3	127	2	R082268	Crystallized recombinant human granulocyte-macrophage colony-stimulating factor.	6.00e-70
24	857	85.0	127	1	P22725	Human Tamm-Horsfall protein.	1.16e-70

		Sequence of human gta	Sequence of human gta
25	85.0	1.32	P/0.363
26	84.8	84.1	R23360
27	84.8	84.1	R20114
			0.77
			0.55
			0.55

IL-3/GM-CSF fusion pr 8.43e-69
IL-3/GM-CSF fusion pr 8.02e-68

31	841	83.4	271	2	R11066	GM-CSF/IL-3 fusion pr	3.93e-68
32	841	83.4	271	4	R23851	GM-CSF/IL-3 fusion pr	3.93e-68
33	841	83.4	271	3	R20113	Human GM-CSF/IL-3 fus	3.93e-68
34	841	83.4	271	5	R23359	PIXY 321	3.93e-68

				CaGM-CSF.	CHEF 2.
39	767	76.1	144	10	R5/8198
40	752	74.6	144	5	R25/699
41	418	41.5	118	3	P50/294
					Sequence of mammalian
					3.32e-28

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RESULT 1
 ID P81886 standard; protein; 144 AA.
 AC P81886;
 DT 29-DEC-1990 (first entry)
 DE Sequence of human granulocyte macrophage colony stimulating factor

KW Lymphokine; interleukin-3; cancer therapy.
OS *Homo sapiens.*

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```

region 1.1
FT /note="Region R1"
FT Region 54..56
FT /note="Region R2"
PN W08805786.A.
PD 11-AUG-1988.
PF 05-FEB-1988; U00335.
PR 06-FEB-1987; US-011794.
PA (GENE-) Genetics Inst.
PI Clark SC, Wong GC, Donahue RE;
    WPT; 88-231549/33.
DR N/P/SDB; NB2353.
DR Colony stimulating factors having reduced carbohydrate levels -

```

PT sequences
PS Disclosure; Table 1, Page 6; 32PP; English.

CC Proteins characterised by possessing GM-CSF-type biological activity
 CC and having specified peptide sequence, except that 1-6 AAs are replaced
 CC and/or deleted within regions Asn-27 - Ser-29 and Asn-37 - Thr-39, such
 CC that one or both of the regions are completely deleted or replaced by a
 CC single AA residue, a dipeptide or a tripeptide sequence other than
 CC Asn-X-Ser or Asn-X-Thr, where X = any AA except for Pro is claimed. Also
 CC claimed are cDNA encoding proteins. Variants are active CSFs which may
 CC be produced in more homogeneous form and which may possess improved
 CC pharmacokinetic profiles relative to natural or recombinant GM-CSF.
 SQ Sequence 144 AA;

Query Match 100.0%; Score 1008; DB 2; Length 144;

Best Local Similarity 95.8%; Pred. No. 3 92e-84;
 Matches 137; Conservative 0; Mismatches 6; Indels 0; Caps 0;

Db 1 mwlgslillgtvacisapsrspsrpsewhvnaiqearrlnlrsrdtaeinetevrv 60

Qy 1 mwlgslillgtvacisapsrspsrpsewhvnaiqearrlnlrsrdtaexnetevrx 60

Db 61 semdliqeptclqrlykqgqsltklkgpltmashyqkhpptpetscatqxitf 120

Qy 61 semdliqeptclqrlykqgqsltklkgpltmashyqkhpptpetscatqxitf 120

Db 121 esfkenlkdfllvipfdcwepvq 143

Qy 121 esfkenlkdfllvxpfcdcwepvq 143

RESULT 3

ID R71118 standard; Protein; 144 AA.

AC R71118;

DT 12-OCT-1995 (first entry)

DE GM-CSF encoded by clone pCD-human-GM-CSF cDNA insert.

KW Human; granulocyte-macrophage colony stimulating factor; GM-CSF;

KW E.coli; quaternary amino ethyl anion exchange chromatography;

KW red 120 triazinyl dye-ligand affinity chromatography; stimulation;

KW gel filtration column chromatography; stimulation; blood cell.

OS Homo sapiens.

PN US5391706-A.

PD 21-FEB-1995.

PF 16-JUL-1987; 074410.

PR 16-JUL-1987; US-074410.

PR 15-DEC-1989; US-055453.

PR 14-APR-1992; US-070153.

PR 21-SEP-1993; US-125356.

PA (SCHERING-PLOUGH CORP.

PI Kosecki RA, Reichert P, Seelig GF, Trotta PP;

DR WPI; 95-09816/13.

DR N-PSDB; Q84865.

PT Purifying granulocyte-macrophage colony-stimulating factor - by

PT anion-exchange, dye-ligand affinity, gel filtration and

PT reversed-phase chromatography.

PS Disclosure: Column 3-4; 5pp; English.

CC This sequence represents human granulocyte-macrophage colony stimulating

CC factor (GM-CSF). Heterogeneity of the nucleotide sequence and the

CC amino acid sequence has been observed and this sequence was deposited

CC in E.coli as ATCC 39223. The GM-CSF protein was isolated using the

CC method of the invention. The method comprises killing and disrupting

CC GM-CSF-expressing bacteria and preparing a GM-CSF containing extract

CC from the disrupted cells. This extract is subjected to quaternary amino

CC ethyl (QAE) anion exchange chromatography to separate proteases and

CC produce protease-free GM-CSF fractions. These fractions are subjected

CC to red 120 triazinyl dye-ligand affinity chromatography to obtain

CC GM-CSF containing fractions free of hydrophobic impurities. These

CC fractions are then subjected to gel filtration column chromatography to

CC produce GM-CSF containing fractions free of high and low mol. wt.

PT impurities which are then subjected to reversed-phase column

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5

CC chromatography to produce fractions with a purity of greater than 95%.
 CC The obtained GM-CSF may be used in clinical situations where the
 CC stimulation of blood cell generation is desirable.
 SQ Sequence 144 AA;

Query Match 99.4%; Score 1002; DB 13; Length 144;
 Best Local Similarity 95.1%; Pred. No. 1.48e-83;
 Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 Db 1 mwlsllllgtvacisaparspspstqpwehnaiqearrllnsrdtaemmetvevi 60
 Qy 1 mwlsllllgtvacisapxpspsqpwehnaiqearrllnsrdtaexnvetvx 60
 .
 Db 61 semfdlgeptclqrtrleykgqlgsitkkgpttmashykhcpptpetscatqitf 120
 Qy 61 semfdlgeptclqrtrleykgqlgsitkkgpttmashykhcpptpetscatqitf 120
 .
 Db 121 esfkenlkdfllivipfdcwepvq 143
 Qy 121 esfkenlkdfllivpxfdcwepvq 143

RESULT 4

ID P6018 standard; protein; 144 AA.
 AC P6018;

DE 01-FAN-1980.; (first entry)

Human granulocyte macrophage-colony stimulating factor.
 Granulocyte; macrophage; colony stimulating factor; chemotherapy;
 PT Human disease therapy; infectious disease therapy; ss.

KW Homo sapiens.

OS N0803225.A.

PD 05-UN-1986.

PF 18-NOV-1985; U02250.

PR 20-NOV-1984; US-73898.

PA (SCH) SCHERING BIOTECH CO.

DR WPI; 86-155831/24.

DR N-PDB; NG0364.

PT New poly:peptide(s) for colony stimulation of granulocytes -
 useful for enhancing body defences against neoplasms and
 PT suppression in PT infectious diseases and to overcome myelo-suppression in
 PT chemotherapy

PS Disclosure: Fig. 1; 53pp; English.

CC The protein has GM-CSF activity and is useful in elucidating
 control mechanisms of mammalian immune responses. It is also
 useful for administration to enhance natural defences against
 neoplastic and infectious diseases or as an adjunct in chemotherapy
 to overcome myelosuppression. GM-CSF is prepared by conventional
 recombinant DNA techniques. The factor has activity on
 human neutrophilic granulocytes, macrophages and eosinophils.

SQ Sequence 144 AA;

Query Match 99.4%; Score 1002; DB 3; Length 144;

Best Local Similarity 95.1%; Pred. No. 1.48e-83;

Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlsllllgtvacisaparspspstqpwehnaiqearrllnsrdtaemmetvevi 60

Qy 1 mwlsllllgtvacisapxpspsqpwehnaiqearrllnsrdtaexnvetvx 60

.
 Db 61 semfdlgeptclqrtrleykgqlgsitkkgpttmashykhcpptpetscatqitf 120

Qy 61 semfdlgeptclqrtrleykgqlgsitkkgpttmashykhcpptpetscatqitf 120

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6

Query Match 99.4%; Score 1002; DB 13; Length 144;
 Best Local Similarity 95.1%; Pred. No. 1.48e-83;
 Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 Db 1 esfkenlkdfllivipfdcwepvq 143
 Qy 121 esfkenlkdfllivpxfdcwepvq 143

RESULT 5

ID P10657 standard; protein; 144 AA.
 AC P10657;

DT 18-APR-1991 (first entry)

DE Sequence of a human granulocyte-macrophage colony stimulating factor (GM-CSF)-like polypeptide isolated from 5637 cell line.

DE AIDS therapy; leucocyte; leukaemia.

KW Homo sapiens.

FH Key location/Qualifiers

FT Cleavage-site 17..18

FT /note= "for signal peptide"

PN N08702060-A.

PD 09-ABR-1987.

PF 03-OCT-1986; U02106.

PR 03-OCT-1985; US-783414.

PA (BIO) BIOPEN NV.

PA (DELMAR) DELAMARTER J.

PI Delamarter J, Ernst JF;

DR WPI; 87-108701/15.

DR N-PSDB; N71002.

PT Human granulocyte-macrophage stimulating factor-like polypeptide(s) - produced from recombinant DNA sequence having 5' terminal alteration

PS Example; Fig 2; 61pp; English.

CC A recombinant DNA molecule encoding a GM-CSF is claimed wherein there is 5' terminal alteration allowing higher yield than the native DNA sequence. The cDNA may be used to reduce the likelihood of infections in immunologically compromised individuals, such as those suffering from AIDS by increasing their white blood cell count.

SQ Sequence 144 AA;

Query Match 99.4%; Score 1002; DB 2; Length 144;

Best Local Similarity 95.1%; Pred. No. 1.48e-83;

Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlsllllgtvacisaparspspstqpwehnaiqearrllnsrdtaemmetvevi 60

Qy 1 mwlsllllgtvacisapxpspsqpwehnaiqearrllnsrdtaexnvetvx 60

.
 Db 61 semfdlgeptclqrtrleykgqlgsitkkgpttmashykhcpptpetscatqitf 120

Qy 61 semfdlgeptclqrtrleykgqlgsitkkgpttmashykhcpptpetscatqitf 120

.
 Db 121 esfkenlkdfllivipfdcwepvq 143

Qy 121 esfkenlkdfllivpxfdcwepvq 143

RESULT 6

ID R04098 standard; protein; 144 AA.
 AC R04098;

DT 10-SEP-1990 (first entry)

DE Metacycrocetase gene product.

KW Metacycrocetase; GM-CSF; leukopenia; osteomyelodysplasia;

KW Granulocyte macrophage colony stimulating factor; ds.

OS Homo sapiens.

PN J02016596-A.

PD 15-MAR-1990.

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CC Asn-X-Ser or Asn-X-Thr, where X = any AA except for Pro is claimed. Also
 CC claimed are cDNA encoding proteins. Variants are active CSFs which may
 CC be produced in more homogenous form and which may possess improved
 CC pharmacokinetic profiles relative to natural or recombinant GM-CSF.
 SQ Sequence 144 AA;

Query Match 99.4%; Score 1002; DB 2; Length 144;
 Best Local Similarity 95.1%; Pred. No. 1.48e-83;
 Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwIqsllllgtvacisaparspsptcpwehnvaiqearrlnlrsdtaaemnetvevi 60
 Qy 1 mwIqsllllgtvacisapxrspsxpwehnvaiqearrlnlrsdtaaexnetvevx 60

Db 61 semfdlqptclqrtrlelykqqlrgalklkqptmmashyqhcptptscatqtif 120
 Qy 61 semfdlqptclqrtrlelykqqlrgalklkqptmmashyqhcptptscatqtif 120

Db 121 esfkenlkdfllvipfdcwepvq 143
 Qy 121 esfkenlkdfllvipfdcwepvq 143

Db 61 semfdlqptclqrtrlelykqqlrgtsitklkqpttumashykhcpcptptscatqtif 120
 Qy 61 semfdlqptclqrtrlelykqqlgsitklkqpttumashykhcpcptptscatqtif 120

Db 121 esfkenlkdfllvipfdcwepvq 143
 Qy 121 esfkenlkdfllvipfdcwepvq 143

RESULT 8
 ID P80567 standard; protein; 144 AA.
 AC P80527;
 DT 24-Oct-1990 (first entry)
 DE Granulocyte macrophage colony stimulating factor.
 KW Granulocyte macrophage colony stimulating factor;
 KW cell line U937; ssDNA.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc-difference 18
 FT /label=Ala
 FT /note="N-terminal residue of mature hGM-CSF"
 FT Misc-difference 97
 FT /label=Ile
 FT /note="differs from residue in hGM-CSF from Mo cells"
 PN EP-281069-A.

PD 07-SEP-1988.
 PF 01-MAR-1988; 103067.
 PR 02-MAR-1987; JP-048580.

PA (SUMO) Sumimoto Pharm KK.
 PI Nakayama C, Okamoto M, Yanagi H;
 DR NPI; 88-251666/36.
 DR N-PSDB; N81118.

PT Human granulocyte-macrophage colony stimulating factor
 PT - produced in human cells transfected with exogenous
 Disclosure; Pt: English.
 CC The sequence is that of human granulocyte macrophage colony
 CC stimulating factor (hGM-CSF) derived from the human cell
 CC line U937. The hGM-CSF is useful for the treatment of
 CC infectious diseases or leukocytopenia which are caused by
 CC e.g. irradiation therapy or chemotherapy. See also P80527.
 SQ Sequence 144 AA;

Query Match 98.5%; Score 993; DB 1; Length 144;
 Best Local Similarity 94.4%; Pred. No. 1.08e-82;
 Matches 135; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwIqsllllgtvacisaparspsptcpwehnvaiqearrlnlrsdtaaemnetvevi 60
 Qy 1 mwIqsllllgtvacisapxrspsxpwehnvaiqearrlnlrsdtaaexnetvevx 60

Db 61 semfdlqptclqrtrlykggrgsltklkp[tmashykhcppt]petscatqitf 120
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Qy 61 semfdlqptclqrtrlykggrgsltklkp[tmashykhcppt]petscatqitf 120
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Kw haemopoiesis; depressed blood cells.

Db 121 esfkenlkdfllvlpfdcwepvq 143
 |||||||:|||||:
 Qy 121 esfkenlkdfllvlpfdcwepvq 143
 |||||||:|||||:

^ RESULT 9
 ID P7056 standard; Protein; 144 AA.
 AC P7056;
 ^ DT 18-APR-1991 (first entry)
 ^ DE Sequence of a human granulocyte-macrophage colony stimulating factor (hGM-CSF)-like polypeptide isolated from U937 cell line.
 DE AIDS therapy; leukocyte; leukaemia.
 KW Human granulocyte-macrophage colony stimulating factor - used eg for
 Homo sapiens.
 FH Key Location/Qualifiers
 FT Cleavage-site 17..18
 FT /note= "for signal peptide"
 FT Misc difference 116
 FT /label= Thr in Mo-cell deriv. cDNA
 PN W08102060-A.
 PD 09-APR-1987.
 PF 03-OCT-1986; U02106.
 PR 03-OCT-1985; US-783414.
 PA (BIOJ) BIOGEN NV.
 PA (DELM) DELAMARER J.
 PI Delamarter J, Ernst JE;
 DR WPI; 87-108701/15.
 DR N-PSDB; NT1001.

PT Human granulocyte-macrophage stimulating factor-like polypeptide(s) - produced from recombinant DNA sequence having 5' terminal alteration
 PT Example; Fig 1; 61BP; English.
 CC A recombinant DNA molecule encoding a hGM-CSF is claimed wherein there is a 5' terminal alteration allowing higher yield than the native DNA sequence. The cdps. may be used to reduce the likelihood of infections in immunologically compromised individuals, such as those suffering from AIDS by increasing their white blood cell count.

SQ Sequence 144 AA;

PT Human granulocyte-macrophage stimulating factor-like polypeptide(s) - produced from recombinant DNA sequence having 5'
 PT terminal alteration
 CC Example; Fig 1; 61BP; English.
 CC A recombinant DNA molecule encoding a hGM-CSF is claimed wherein there is a 5' terminal alteration allowing higher yield than the native DNA sequence. The cdps. may be used to reduce the likelihood of infections in immunologically compromised individuals, such as those suffering from AIDS by increasing their white blood cell count.

SQ Sequence 144 AA;

Query Match 98.5%; Score 993; DB 2; Length 144;
 Best Local Similarity 94.4%; Pred. No. 1.0le-02;
 Matches 135; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlqlillgtvacisaparspspsqpwvhnaigearrlnlrsdtaaemnetvevi 60
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 Qy 1 mwlqlillgtvacisaparspspsqpwvhnaigearrlnlrsdtaaemnetvevi 60
 |||||||:|||||:
 Db 61 semfdlqptclqrtrlykggrgsltklkp[tmashykhcppt]petscatqitf 120
 |||||||:|||||:
 Qy 61 semfdlqptclqrtrlykggrgsltklkp[tmashykhcppt]petscatqitf 120
 |||||||:|||||:
 Db 121 esfkenlkdfllvlpfdcwepvq 143
 |||||||:
 Qy 121 esfkenlkdfllvlpfdcwepvq 143
 |||||||:

RESULT 10
 ID P9485 standard; protein; 142 AA.
 AC P9485;
 ^ DT 21-APR-1991 (first entry)
 ^ DE Sequence of granulocyte macrophage colony stimulating factor (GM-CSF) in plasmid PHC3.
 DE Cancer therapy; tumoricide.
 KW Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 2..13
 FT Protein 14..397
 PN EP-211684-A.
 PD 25-FEB-1987.
 PF 15-AUG-1986; 306304.

DT 27-JUN-1989 (first entry)
 DE Human granulocyte macrophage colony stimulating factor polypeptide.
 KW Human granulocyte macrophage colony stimulating factor (GM-CSF);
 KW haemopoiesis; depressed blood cells.

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 33..464
 FT PolyA signal 780..787
 PN EP-299782-A.
 PD 18-JUN-1989.
 PF 15-JUL-1987; US-074988.

PA (SCHERING) Schering Biotech. Co.
 PI Yokota T, Lee FD, Remnick DM, Arai K-I, Arai N.
 DR WPI; 89-017271/03.

DR N-PSDB; N93172.
 PT Human granulocyte macrophage colony stimulating factor - used eg for
 PT haemopoiesis stimulation and used in treating depressed blood cell
 PT populations.
 PT Disclosure; fig.1; 40pp; English.

PS Corresponding cDNA sequence is inserted into an expression vector contg.
 CC eg SV40 origin, pref. also a bacterial origin, SV40 early- and SR alpha
 CC promoters,etc. The resulting library is screened and colonies selected
 CC which produce GM-CSF (i.e. those contg. plasmid pcd-human-GM-CSF). Modif-
 CC ed forms of GM-CSF are made by producing mutant forms of cDNA esp. using
 CC cassette mutagenesis. These mutants can be glycosylated or non-glycosyl-
 CC ated, substd.(1-2 fold), deleted (1-fold) or inserted (1-fold) forms of
 CC GM-CSF. GM-CSF is useful in the treatment of myeloid hypoplasia and stim-
 CC ulates regeneration of the haematopoietic system following eg bone marrow
 CC transplants and some cancer treatments. Mutant forms show reduced side
 CC effects, improved stability towards proteases and increased yields.
 SQ Sequence 142 AA;

Query Match 96.8%; Score 976; DB 2; Length 142;
 Best Local Similarity 94.4%; Pred. No. 4.63e-81;
 Matches 135; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Db 1 mw1qlillgtvacisaparspspsqpwvhnaigearrlnlrsdtaaemnetvevi 58
 |||||||:|||||:
 Qy 1 mw1qlillgtvacisaparspspsqpwvhnaigearrlnlrsdtaaemnetvevi 60
 |||||||:|||||:
 Db 59 semfdlqptclqrtrlykgprqsltklkp[tmashykhcppt]petscatqitf 118
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 Qy 61 semfdlqptclqrtrlykgqlqsltklkp[tmashykhcppt]petscatqitf 120
 |||||||:|||||:
 Db 119 esfkenlkdfllvlpfdcwepvq 141
 |||||||:
 Qy 121 esfkenlkdfllvlpfdcwepvq 143
 |||||||:

RESULT 11
 ID P7031 standard; Protein; 131 AA.
 AC P7031;
 ^ DT 21-APR-1991 (first entry)
 ^ DE Sequence of granulocyte macrophage colony stimulating factor
 DE (GM-CSF) in plasmid PHC3.
 DE Cancer therapy; tumoricide.
 KW Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 2..13
 FT Protein 14..397

PN EP-211684-A.
 PD 25-FEB-1987.
 PF 15-AUG-1986; 306304.

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PR 16-AUG-1985; US-768893.
 PR 16-AUG-1985; US-768893.
 PR 31-JUL-1986; US-888995.
 PA (IMMUNEX CORP.
 PI Anderson DM, Cantrell MA, Garretti DP, Conlon PJ, Cosman DJ,
 PI Grabstein KH, Larsen AD, Price VL;
 DR WPI; 87-051818/08.

PT Activating macrophage tumoricidal activity for cancer treatment -
 PT by treating with granulocyte macrophage colony stimulating factor
 Disclosure; Fig 1; 27pp; English.
 * CC When used for cancer treatment, the cells are pref. isolated,
 treated in vitro with GM-CSF, then returned to the patient so as to
 inactivate tumor cells, or administered directly. GM-CSF is pref.
 purified to specific activity at least 1.5 x 1million CFU /microgram
 protein. Pref. the cells being treated are derived from peripheral
 blood monocytes, and 0.01-100ng GM-CSF is used per 2 x 100 000 cells.
 Sequence 131 AA;

Query Match 89.2%; Score 899; DB 2; Length 131;
 Best Local Similarity 94.6%; Pred. No. 1.11e-73;
 Matches 123; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 SQ

Db 1 csiaparpspsqpehvnaiqearrlnlsdaemnetveisemfdlqepctcq 60
 Qy 14 csiapxrpssqpehvnaiqearrlnlsdaexnetvxsemfdlqepctcq 73

Db 61 trileykqglgsitk1kgpltmashykgchcpptpetscatqitfeskenlkdfllv 120
 Qy 74 trileykqglgsitk1kgpltmashykgchcpptpetscatqitfeskenlkdfllv 133

Db 121 ipfdcwepvq 130
 Qy 134 xpfdcwepvq 143

RESULT 12
 ID P60350 standard; protein; 131 AA.
 AC P60350;
 DT 01-AUG-1991 (first entry)
 DE Human granulocyte macrophage colony stimulating factor.
 KW Human granulocyte macrophage colony stimulating factor; ss DNA;
 OS Homo sapiens.
 EH Location/Qualifiers
 FT Protein 5..131
 FT /label=mature protein
 PN EP-183350-A.
 PD 04-JUN-1986.
 PF 25-SEP-1985; 306827.
 PR 29-OCT-1984; US-666041.
 PR 02-JUL-1985; US-754041.
 PA (IMMUNEX CORP.
 PI Anderson DM, Cantrell MA, Garretti DP, Cosman DJ, Larsen AD;
 PI Price VL;
 DR WPI; 86-145553/23.
 PT New DNA encoding for expression of human colony stimulating
 factor - useful in prodn. of the factor, esp. granulocyte
 macrophage factor, for treating leukaemia and in bone marrow
 transplantation
 Disclosure; Fig 2; 34pp; English.
 CC leukaemia; anaemia; bone marrow transplantation
 CC Human granulocyte macrophage colony stimulating factor can be
 produced in large amts. In homogeneous form it is useful in the
 possible treatment of proliferative blood disorders, eg certain

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CC leukemias and anemias. GM-CSF of greater purity and in larger
 amounts may be useful in bone marrow transplantation after cancer
 therapy.
 Sequence 131 AA;

Query Match 88.8%; Score 895; DB 3; Length 131;
 Best Local Similarity 93.8%; Pred. No. 2.69e-73;
 Matches 122; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 SQ

Db 1 csiaparpspsqpehvnaiqearrlnlsdaemnetveisemfdlqepctcq 60
 Qy 14 csiapxrpssqpehvnaiqearrlnlsdaexnetvxsemfdlqepctcq 73

Db 61 trileykqglgsitk1kgpltmashykgchcpptpetscatqitfeskenlkdfllv 120
 Qy 74 trileykqglgsitk1kgpltmashykgchcpptpetscatqitfeskenlkdfllv 133

Db 121 ipfdcwepvq 130
 Qy 134 xpfdcwepvq 143

RESULT 13
 ID R41510 standard; protein; 127 AA.
 AC R41510;
 DT 16-MAR-1994 (first entry)
 DE r-h-GM-CSF.
 KW Recombinant; human; granulocyte macrophage colony stimulating factor;
 KW r-h-GM-CSF; GM-CSF; crystals; polyethylene glycol; PBS; activity;
 KW myelodysplasia syndromes; AIDS; cancer.
 OS Homo sapiens.
 PN EP-561429-A.
 PD 22-SEP-1993.
 PF 04-JUN-1990; 306042.
 PR 06-JUN-1989; US-362187.
 (SCHE) SCHERING CORP.
 PA PI Hammond GS, Le HV, Nagabushan TL, Reichert P, Trotta PP;
 DR WPI; 93-29672B/38.
 PT Prep. of crystalline granulocyte-macrophage colony-stimulating
 factor - ovid. by equilibrating soln. contg. GM-CSF and
 PT polyethylene glycol, used for treating myelodysplasia syndromes,
 PT AIDS and cancer
 PS Disclosure; Page 3; 6pp; English.
 CC This sequence represents recombinant human granulocyte macrophage
 CC colony stimulating factor (r-h-GM-CSF). Crystals of this protein
 CC were produced using the method of the invention. This method
 CC comprises equilibrating solution of GM-CSF against a solution that
 CC causes the solution of GM-CSF to become more concentrated and to
 CC form GM-CSF crystals, where the equilibrated solution of GM-CSF
 CC contains polyethylene glycol (PEG) with a molecular weight of 8,000
 CC and 40-250 mg/ml of GM-CSF. The crystalline GM-CSF retains all full
 CC activity so that upon redissolution in an aq. system it possessed the
 CC same activity as the GM-CSF starting material used in preparing the
 CC crystals. The GM-CSF can be used for the treatment of myelodysplasia
 CC syndromes, AIDS and cancer.
 SQ Sequence 127 AA;

Query Match 86.4%; Score 871; DB 8; Length 127;
 Best Local Similarity 94.4%; Pred. No. 5.33e-71;
 Matches 119; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 SQ

Db 1 aparspspsqpehvnaiqearrlnlsdaemnetveisemfdlqepctcq 60
 Qy 18 apxrspssqpehvnaiqearrlnlsdaexnetvxsemfdlqepctcq 77

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Db 61 lykqglqsltklqpitmmashykhcpotpetscatqitfesthenlkdfllvifid 120
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 78 lykqglqsltklqpitmmashykhcpotpetscatqitfesthenlkdfllvifd 137
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 cwepvq 126
|||:
Qy 138 cwepvq 143
|||:
RESULT 14

* ID R13215; standard; protein; 127 AA.
* AC R13215;
* DT 10-OCT-1991 (first entry)
* DE Oxidised GM-CSF
* KW Granulocyte-macrophage colony stimulating factor; AIDS;
bone marrow transplantation;
OS Homo sapiens.

FH Key Location/Qualifiers

FT Modified -site 36
FT /note= "oxidised"
FT Modified -site 46
FT /note= "oxidised"
FT Modified -site 79
FT /note= "oxidised"
FT Modified -site 80
FT /note= "oxidised"
PN W0910684-A.
PD 25-JUL-1991.
PF 04-JAN-1991; U00007.
PR 08-JAN-1990; US-462180.
PA (SCH) SCHERING CORP.
PI Reichert P, Seelig GF, Trotta PP;
DR WPI; 91-237988/32.

PT Oxidised GM-CSF with oxidised methionine residues - for treatment of AIDS, myelodysplastic syndrome, etc.
PS Disclosure; Fig 1; 36pp; English.
CC The GM-CSF variants have at least one of the methionine residues oxidised and are free of unoxidised GM-CSF and other oxidised variants. They possess a significant amt. of the biological activity of unoxidised GM-CSF but some of them have different receptor binding characteristics. They may have different pharmacokinetic properties in vivo and greater stability and resistance to proteolytic degradation and clearance in vivo. The variants may be used as for unoxidised GM-CSFs, e.g., for treating AIDS, myelodysplastic syndrome or for bone marrow transplantation. Because the biological activity of the most highly oxidised variant is much lower than that of the other variants or of unoxidised GM-CSF, it could be useful as an antagonist.
CC The prod. may be obt. by treating unoxidised GM-CSF with an oxidising agent or can be isolated from natural sources or from recombinant DNA expression systems.
SQ Sequence 127 AA;

Query Match 86.4%; Score 871; DB 3; Length 127;
Best Local Similarity 94.4%; Pred. No. 5.33e-71;
Matches 119; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Db 1 aparspspstpcwvhnaigearrlnlrsdaemnetrevsemfdlgeptclqrle 60
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Qy 18 apxspsspxpcwvhnaigearrlnlrsdaemnetrevsemfdlgeptclqrle 77
|||:
Db 61 lykqglqsltklqpitmmashykhcpotpetscatqitfesthenlkdfllvifd 120
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 78 lykqglqsltklqpitmmashykhcpotpetscatqitfesthenlkdfllvifd 137
|||:
Db 121 cwepvq 126
|||:
Qy 138 cwepvq 143
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RESULT 15

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Qy 78 lykqglqsltklqpitmmashykhcpotpetscatqitfesthenlkdfllvifd 137
|||:
Db 121 cwepvq 126
|||:
Qy 138 cwepvq 143
|||:
ID R33774; standard; protein; 127 AA.
AC R33774;
* DT 27-JUL-1993 (first entry)
* DE Recombinant human Granulocyte Macrophage-Colony Stimulating Factor;
KW rhGM-CSF; freeze-dried composition; lyophilisation; neutropenia.
* OS Homo sapiens.
PN W09305799-A.
* PD 01-APR-1993.
* PF 10-SEP-1992; E02084.
* PR 24-SEP-1991; GB-020304.
* PA (FARM) FARMITALIA ERBA SRL CARIO.
* PI Cavallo A, Dalla CASA R, Magrini R, Nella L;
* DR WPI; 93-117243/14.
* PT Stable Lyophilised compen. for treating e.g. neutropenic disorders of cancer patients after chemotherapy - comprises granulocyte macrophage colony stimulating factor, bulking agent, polyoxyethylene sorbitan fatty acid ester and basic amino acid
* PT Claim 7; Page 22; 24pp; English.
* CC The GM-CSF used in lyophilised compositions of the invention is pref. recombinant human GM-CSF having the sequence R33774 or is the Leu23-GM-CSF mutant Q33T75. The GM-CSF is pref. present in an amount 0.1-1 wt.% of the bulking agent. Lyophilised (freeze-dried) compositions containing proteins are more stable than unlyophilised compsns. The compn. containing GM-CSF is useful for treating neutropenic disorders of cancer patients after chemotherapy.
SQ Sequence 127 AA;

Query Match 86.4%; Score 871; DB 7; Length 127;
Best Local Similarity 94.4%; Pred. No. 5.33e-71;
Matches 119; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
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|||:||||:||||:||||:||||:||||:||||:||||:
Qy 18 apxspsspxpcwvhnaigearrlnlrsdaemnetrevsemfdlgeptclqrle 77
|||:
Db 61 lykqglqsltklqpitmmashykhcpotpetscatqitfesthenlkdfllvifd 120
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Qy 78 lykqglqsltklqpitmmashykhcpotpetscatqitfesthenlkdfllvifd 137
|||:
Db 121 cwepvq 126
|||:
Qy 138 cwepvq 143
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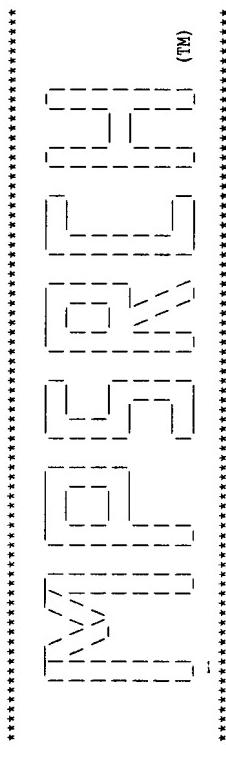
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Release 2.1D John F. Collins, Biocomputing Research Unit.

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MPsrch.DP Protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 21 12:19:26 1996; MasPar time 6.88 Seconds

528.733 Million cell updates/sec

Tabular output not generated.

Title: >p60535

Description: (1-144) from p60535.pep

Perfect Score: 1008

Sequence: 1 mwlsllllgtvacsisapx.....enlkdflllxpxfdewepvqx 144

Scoring table: PAM 150

Gap 11

Searched: 82306 seqs, 25270970 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: pir46

1.unann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unrev1
13:unrev2

Statistics: Mean 41.316; Variance 95.998; scale 0.430

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description Pred. No.

Result No.	Score	Query	Match	Length	DB ID	Description	Pred. No.
1	1002	99.4	144	2	FOHGM	granulocyte-macrophage	3.80e-153
2	828	82.1	144	5	JH0469	granulocyte-macrophage	5.21e-122
3	821	81.4	144	11	A61632	granulocyte-macrophage	9.19e-121
4	73	76.7	143	2	F0BGM	granulocyte-macrophage	3.14e-112
5	752	74.6	144	5	A4936	granulocyte-macrophage	1.67e-108
6	546	54.2	141	5	A24644	granulocyte-macrophage	2.53e-72
7	536	53.2	141	5	A24636	granulocyte-macrophage	1.37e-70
8	416	41.3	118	2	F0MGM	granulocyte-macrophage	5.37e-50
9	102	10.1	605	6	S33019	hypothetical protein	2.16e-01
10	102	10.1	605	3	Q0BE29	BRLF1 protein - huma	2.16e-01
11	100	9.9	581	4	S50769	alpha-glucosidase ho	3.70e-01
12	97	9.6	146	10	D42402	cell surface glycopr	8.21e-01

RESULT	ENTRY	TITLE	FOHGM	TYPE
1			granulocyte-macrophage	complete
			human	
			colony-stimulating factor 2; GM-CSF	
			#common_name man	
			04-Dec-1996 #sequence_revision 04-Dec-1996 #text_change	
			18-Aug-1995	
			C24636; A25169; A01853; A44175; JC1090	
			A91015	
			REFERENCE	
			#authors	
			#journal	
			#title	
			Structure of the chromosomal gene for granulocyte-macrophage	
			colony stimulating factor: comparison of the mouse and	
			human genes.	
			#cross-references MVID:86030234	
			#accession C24636	
			#molecule_type DNA	
			#residues 1-144 #label MIY	
			#cross-references EMBL:X03021	
			A51169	
			Cantrell, M.A.; Anderson, D.; Cerretti, D.P.; Price, V.;	
			McKereghan, R.; Tushinski, R.J.; Mochizuki, D.Y.; Larsen,	
			A.; Grabstein, K.; Gillis, S.; Cosman, D.	
			Proc. Natl. Acad. Sci. U.S.A. (1985) 82:6250-6254	
			Cloning, sequence, and expression of a human	
			granulocyte-macrophage colony-stimulating factor.	

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#cross-references MUID:85298329
#accession A25169
#molecule_type mRNA
#residues 1-144 #label CAN
#cross-references GB:MI11734
REFERENCE A01953
#authors Lee, F.; Yokota, T.; Otsuma, T.; Gemelli, L.; Larson, N.; Luh, J.; Arai, K.; Rennick, D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1985) 82:4360-4364
#title Isolation of cDNA for a human granulocyte-macrophage colony-stimulating factor by functional expression in mammalian cells.
#cross-references MUID:85242684
#accession A01953
#molecule_type mRNA
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#cross-references GB:MI11220
REFERENCE A44175
#authors Wong, G. C.; Wittek, J. S.; Temple, P. A.; Wilkins, K. M.; Leary, A. C.; Luxenberg, D. P.; Jones, S. S.; Brown, E. L.; Kay, R. M.; Orr, E. C.; Shoemaker, C.; Colde, D. W.; Kaufman, R. J.; Hawick, R. M.; Wang, E. A.; Clark, S. C.
#journal Science (1985) 238:810-815
#title Human GM-CSF: molecular cloning of the complementary DNA and purification of the natural and recombinant proteins.
#cross-references GB:MI0663
#accession A44175
#molecule_type mRNA
#residues 1-116, 'T', 118-144 #label WGN
#cross-references GB:MI0663
#note parts of this sequence, including the amino end of the mature protein, were confirmed by peptide sequencing
REFERENCE JC1090
#authors Wen, D. Y.; Huang, B. R.; Cai, L. W.; Si, J. Y.
#journal Acta Biochim. Biophys. Sin. (1993) 25:631-635
#title Amplification of human granulocyte-macrophage colony-stimulating factor cDNA with the method of reverse transcript-polymerase chain reaction.
#cross-references GB:MI0663
#accession JC1090
#status preliminary
#molecule_type protein
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#introns 53/3; 67/3; 109/3
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#classification #superfamily granulocyte-macrophage colony-stimulating factor cytokine; glycoprotein; growth factor; monomer;
#keywords T-cell
FEATURE 1-17
#description stimulates the differentiation and proliferation of hematopoietic progenitor cells into granulocytes, macrophages, and perhaps eosinophils
#classification #superfamily granulocyte-macrophage colony-stimulating factor cytokine; glycoprotein; growth factor; monomer;
#keywords T-cell
18-144
44,54
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Query Match 99.4%; Score 100%; DB 2; Length 144;
Best Local Similarity 95.1%; Pred. No. 3.80e-153;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
#domain signal sequence #status predicted #label SIG
#product granulocyte-macrophage colony-stimulating factor #status experimental #label MATV
#binding site carbohydrate (Asn) (covalent) #status predicted
#length 144 #molecular-weight 16318 #checksum 9541
Query Match 82.1%; Score 828; DB 5; Length 144;
Best Local Similarity 77.6%; Pred. No. 5.21e-122;
Matches 111; Conservative 10; Mismatches 22; Indels 0; Gaps 0;
#domain signal sequence #status predicted #label SIG
#product granulocyte-macrophage colony-stimulating factor #status experimental #label MATV
#binding site carbohydrate (Asn) (covalent) #status predicted
#length 144 #molecular-weight 16318 #checksum 9541
Query Match 82.1%; Score 828; DB 5; Length 144;
Best Local Similarity 77.6%; Pred. No. 5.21e-122;
Matches 111; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

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Qy 121 esfkemlkdfllvipfdcwepvq 143
Db 2 JH0469 #type complete
#label granulocyte-macrophage colony-stimulating factor precursor -
TITLE sheep
ALTERNATE NAMES colony-stimulating factor 2; GM-CSF
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#common_name domestic sheep
DATE 31-Mar-1992 #text_change 18-Jun-1993
ACCESSIONS JH0469; S16730
REFERENCE #authors McInnes, C.J.; Haig, D.M.
#journal Gene (1991) 105:275-279
#title Cloning and expression of a cDNA encoding ovine granulocyte-macrophage colony-stimulating factor.
#cross-references MUID:92039044
#accession JH0469
#molecule_type mRNA
#residues 1-144 #label MCI
#cross-references GB:X53561
COMMENT This protein is a glycoprotein cytokine produced and secreted by various cell types including activated T-cells and macrophages.
CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
#keywords cytokine; glycoprotein; growth factor; monomer; T-cell
FEATURE 1-17
#domain signal sequence #status predicted #label SIG
#product granulocyte-macrophage colony-stimulating factor #status predicted #label MATV
#binding site carbohydrate (Asn) (covalent) #status predicted
#length 144 #molecular-weight 16318 #checksum 9541
Query Match 82.1%; Score 828; DB 5; Length 144;
Best Local Similarity 77.6%; Pred. No. 5.21e-122;
Matches 111; Conservative 10; Mismatches 22; Indels 0; Gaps 0;
Db 1 mwqlqllllgtvacisaparspsptqwehnaiqearrllnlrsdtaaemtvervi 60
Qy 1 mwqlqllllgtvacisaparspspxqwehnaiqearrllnlrsdtaaexnetverx 60
Db 61 semfdqepctlqrlykqqlrlsllkplttmashykhcpptetscatqxitf 120
Qy 61 semfdqepctlqrlykqqlrlsllkplttmashykhcpptetscatqxitf 120
Db 121 ksfkemlkdfllvipfdcwepvq 143
Qy 121 esfkemlkdfllvipfdcwepvq 143
RESULT 3

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A61632 #type complete granulocyte-macrophage colony-stimulating factor precursor - sheep
#formal_name *Ovis orientalis aries*, *Ovis ammon aries*
#common_name domestic sheep
DATE 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 28-Jul-1995

ACCESSIONS A61632
REFERENCE A61632
#authors O'Brien, P.M.; Rothel, J.S.; Seow, H.F.; Wood, P.R.
#journal Immunol. Cell Biol. (1991) 69:51-55
#title Cloning and sequencing of the cDNA for ovine granulocyte-macrophage colony-stimulating factor (GM-CSF).
ACCESSION A61632
#status preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues 1-144 #label OAB

FEATURE 1-17 #domain signal sequence #status predicted #label SIG
#length 144 #molecular-weight 16290 #checksum 8953
SUMMARY Query Match Score 81.4%; Pred. No. 9.19e-121;
Best Local Similarity 76.9%; Matches 110; Conservative 23; Indels 0; Gaps 0;

Db 1 mwlgpllllgtvvccsapsqrpsvtrpqrghdaikealsllndttaaymdetvrrv 60
|||:||||| |||:||| :|||:||| |||:||| :|||:||| :|||:
Qy 1 mwlgpllllgtvvccsapsqrpsvtrpqrghdaikealsllndttaaymdetvrrv 60
|||:||||| |||:||| :|||:||| |||:||| :|||:
Db 61 sekfdisqptclqrtrklykgnglsqtslgmsltmmathvekhcpptpcqtqfis 119
|||:||||| |||:||| :|||:||| |||:||| :|||:
Qy 61 sekfdisqptclqrtrklykgnglsqtslgmsltmmathvekhcpptpcqtqfis 119
|||:||||| |||:||| :|||:||| |||:||| :|||:
Db 120 knfkdellkfifiiipfdcwepaq 142
|||:||||| :|||:||| :|||:
Qy 121 estkenldflivxpfdcwepqv 143
|||:||||| :|||:||| :|||:
RESULT 5
ENTRY A44936 #type complete granulocyte-macrophage colony-stimulating factor, GM-CSF - dog
TITLE #cross-references NCBI:49739
#organism Canis lupus familiaris #common_name dog
#date 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 12-Apr-1995
ACCESSIONS A44936
REFERENCE Nash, R.A.; Schuening, F.; Appelbaum, F.; Hammond, W.P.; Boone, T.; Morris, C.R.; Slichter, S.J.; Storb, R.
#authors Blood (1991) 78:930-937
#journal Molecular cloning and in vivo evaluation of canine granulocyte-macrophage colony-stimulating factor.
#cross-references MUID:91329842
#accession A44936
#status preliminary
#molecule_type mRNA
#residues 1-144 #label NAS
#cross-references NCBI:49738; NCBI:49739
#note sequence derived from NCBI backbone
CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
SUMMARY #length 144 #molecular-weight 16137 #checksum 9761
Query Match Score 74.6%; Pred. No. 1.67e-108;
Best Local Similarity 69.7%; Matches 99; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Db 1 mwlgpllllgtvvccsapsqrpsvtrpqrghdaikealsllndttaaymdetvrrv 60
|||:||||| |||:||| :|||:||| |||:||| :|||:
Qy 1 mwlgpllllgtvvccsapsqrpsvtrpqrghdaikealsllndttaaymdetvrrv 60
|||:||||| |||:||| :|||:||| |||:||| :|||:
Db 61 sevfdisqptclqrtrklykgnglsqtslgmsltmmashykhcpptpcqtqf 120
|||:||||| |||:||| :|||:||| |||:||| :|||:
Qy 61 sevfdisqptclqrtrklykgnglsqtslgmsltmmashykhcpptpcqtqf 120
|||:||||| |||:||| :|||:||| |||:||| :|||:
Db 121 kskenldflivxpfdcwepkv 142
|||:||||| :|||:||| :|||:
Qy 121 estkenldflivxpfdcwepv 142
|||:||||| :|||:||| :|||:
RESULT 4
ENTRY FQBGM #type complete granulocyte-macrophage colony-stimulating factor precursor - bovine
TITLE #cross-references JL0037
#ALTERNATE NAMES
#ORGANISM Bos primigenius taurus #common_name cattle
#DATE 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 27-Jan-1995
ACCESSIONS JL0037
#authors Maliszewski, C.R.; Schoenborn, M.A.; Corretti, D.P.; Wigñall, J.M.; Picha, K.S.; Cosman, D.; Tushinski, R.J.; Gillis, S.; Baker, P.E.
#journal Mol. Immunol. (1988) 25:843-850
#title Bovine GM-CSF: molecular cloning and biological activity of the recombinant protein.
#cross-references MUID:89036971
#accession JL0037
#molecule_type mRNA
#residues 1-143 #label MAL
#COMMENT This glycoprotein induces granulocyte, macrophage, and eosinophil colony formation.
#classification #superfamily granulocyte-macrophage colony-stimulating factor cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
#KEYWORDS
#FEATURE

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RESULT 6 A24644 #type complete
 ENTRY granulocyte-macrophage colony-stimulating factor precursor -
 TITLE mouse

ALTERNATE_NAMES colony-stimulating factor 2; GM-CSF
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change
 18-Jun-1993

ACCESSIONS A24644
 REFERENCE A24644 Delamarre, J.F.; Mermod, J.J.; Liang, C.M.; Eliason, J.F.;
 Thatcher, D.R.
 #journal EMBO J. (1985) 4:2575-2581
 #cross-references PMID:86030236
 #accession A24644
 #molecule_type mRNA
 #residues 1-141 #label DEL
 #classification #superfamily granulocyte-macrophage colony-stimulating factor
 KEYWORDS cytokine; glycoprotein; growth factor; monomer;
 T-cell
 SUMMARY #length 141 #molecular-weight 16090 #checksum 4151

Query Match Score 546; DB 5; Length 141;
 Best Local Similarity 53.1%; Pred. No. 1.37e-70;
 Matches 76; Conservative 20; Mismatches 45; Indels 3; Gaps 1;

Db 1 mw1qnllflgivvyslsaptspitvrpkhveakealnld--dmpvtlineevvv 57
 Qy 1 mw1qslillgtacsissaptspsspsxpwvhvnaigearllnsrdtaexnetvvx 60

Query Match Score 542%; DB 5; Length 141;
 Best Local Similarity 53.1%; Pred. No. 2.53e-72;
 Matches 76; Conservative 20; Mismatches 44; Indels 3; Gaps 1;

Db 1 mw1qnllflgivvyslsaptspitvrpkhveakealnld--dmpvtlineevvv 57
 Qy 1 mw1qslillgtacsissaptspsspsxpwvhvnaigearllnsrdtaexnetvvx 60

Db 58 snefsfkltcvtrkifegqlgnftkikgalnntasyyqtcppptpcdcetavvv 117
 Qy 61 semfdlqptclqrlykgqsgstikkgpttmasiykdhcptscatqitf 120

Db 118 adfidslktfitdpfeckkpvq 140
 Qy 121 esfkenlkdfllvxpfcdewpq 143

RESULT 7 A24636 #type complete
 ENTRY granulocyte-macrophage colony-stimulating factor precursor -
 TITLE mouse

ALTERNATE_NAMES colony-stimulating factor 2; GM-CSF
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change
 14-Sep-1994

ACCESSIONS A24636; A24645
 REFERENCE A91015 Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.
 #authors
 #journal EMBO J. (1985) 4:2561-2568
 #title Structure of the chromosomal gene for granulocyte-macrophage
 colony stimulating factor: comparison of the mouse and
 human genes.

#cross-references PMID:86030236
 #accession A24636
 #molecule_type DNA; mRNA
 #residues 1-141 #label MIY
 #note the sequence translated from the mRNA differs from that
 of the DNA in having 139-Ser

REFERENCE A24645 Stanley, E.; Metcalf, D.; Sobieszczuk, P.; Gough, N.M.; Dunn,
 A.R.

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#journal EMBO J. (1985) 4:2569-2573
 #title The structure and expression of the murine gene encoding
 granulocyte-macrophage colony-stimulating factor: evidence
 for utilisation of alternative promoters.

#cross-references PMID:86030235
 #accession A24645
 #molecule_type DNA
 #residues 1-141 #label STA

GENETICS 50/3; 64/3; 106/3
 #introns
 CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
 KEYWORDS cytokine; glycoprotein; growth factor; macrophage; monomer;
 T-cell
 #length 141 #molecular-weight 16090 #checksum 4151

SUMMARY Query Match Score 53.2%; Score 536; DB 5; Length 141;
 Best Local Similarity 52.4%; Pred. No. 1.37e-70;
 Matches 75; Conservative 20; Mismatches 45; Indels 3; Gaps 1;

Db 1 mw1qnllflgivvyslsaptspitvrpkhveakealnld--dmpvtlineevvv 57
 Qy 1 mw1qslillgtacsissaptspsspsxpwvhvnaigearllnsrdtaexnetvvx 60

Query Match Score 546; DB 5; Length 141;
 Best Local Similarity 53.1%; Pred. No. 2.53e-72;
 Matches 76; Conservative 20; Mismatches 44; Indels 3; Gaps 1;

Db 1 mw1qnllflgivvyslsaptspitvrpkhveakealnld--dmpvtlineevvv 57
 Qy 1 mw1qslillgtacsissaptspsspsxpwvhvnaigearllnsrdtaexnetvvx 60

Query Match Score 542%; DB 5; Length 141;
 Best Local Similarity 53.1%; Pred. No. 2.53e-72;
 Matches 76; Conservative 20; Mismatches 44; Indels 3; Gaps 1;

Db 1 mw1qnllflgivvyslsaptspitvrpkhveakealnld--dmpvtlineevvv 57
 Qy 1 mw1qslillgtacsissaptspsspsxpwvhvnaigearllnsrdtaexnetvvx 60

Db 58 snefsfkltcvtrkifegqlgnftkikgalnntasyyqtcppptpcdcetavvv 117
 Qy 61 semfdlqptclqrlykgqsgstikkgpttmasiykdhcptscatqitf 120

Db 118 adfidslktfitdpfeckkpvq 140
 Qy 121 esfkenlkdfllvxpfcdewpq 143

RESULT 8 F0MSGM #type complete
 ENTRY F0MSGM #type complete
 TITLE granulocyte-macrophage colony-stimulating factor - mouse
 ALTERNATE NAMES colony-stimulating factor 2; GM-CSF
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change
 10-Mar-1994

ACCESSIONS A01854
 REFERENCE A01854
 #authors Gough, N.M.; Gough, J.; Metcalf, D.; Kelso, A.; Grail, D.;
 Nicola, N.A.; Burgess, A.W.; Dunn, A.R.
 #journal Nature (1984) 309:763-767
 #title Molecular cloning of cDNA encoding a murine haematopoietic
 growth regulator, granulocyte-macrophage colony stimulating
 factor.
 #cross-references PMID:84245825
 #accession A01854

#molecule_type mRNA
 #residues 1-118 #label GOU

#cross-references GB:X05906
 COMMENT The mRNA for this protein was isolated from lung tissue.

CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
 KEYWORDS cytokine; glycoprotein; growth factor; macrophage; monomer;
 T-cell

FEATURE 60,69 #binding site carbohydrate (Asn) (covalent) #status
 Predicted
 #length 118 #molecular-weight 13544 #checksum 2606

Query Match Score 41.3%; DB 2; Length 118;
 Best Local Similarity 50.9%; Pred. No. 5.37e-50;
 Matches 59; Conservative 17; Mismatches 31; Indels 3; Gaps 1;

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RESULT	9	S33019	#type complete
ENTRY		hypothetical protein - human herpesvirus 4	
ORGANISM		# formal name human herpesvirus 4, Epstein-Barr virus	
NAME		13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change	

contents annotation; protein coding region

```

RESULT          10      Q0BE29   #type complete
ENTRY          MMLF1 protein - human herpesvirus 4 (strain B95-8)
TITLE          MMLF1 protein - human herpesvirus 4, Epstein-Barr virus
ORGANISM       25-Feb-1985 sequence_revision 25-Feb-1985 #text_change
DATE          31-Dec-1993

```

Journal title Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8. Muri. Divisi. New: \13035 J. Virol. 45: 121-145

```

cross-references MUID:85035713
accession A33043
molecule_type DNA
residues 1-605 #label BAN
REFERENCE A33794

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#authors	journal
Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; Hatfull, G.; Hudson, G.S.; Satchwell, S.C.; Sequin, C.; Tuffnail, P.S.; Barrell, B.G.	Nature (1984) 310:207-211

DNA sequence and genome.

```

RESULT 11
ENTRY S50769 #type complete
TITLE alpha-glucosidase homolog YJ1216c - yeast (Saccharomyces
        cerevisiae)
ORGANISM protein HRF501; protein JU228; protein YJ1216c
ALTERNATE_NAMES #formal name Saccharomyces cerevisiae
DATE 30-Sep-1991 #sequence_revision 08-Sep-1995 #text_change
        13-Sep-1995
ACCESSIONS S50769; S570006; S45157
REFERENCE S50701
AUTHORS Vandembol, M.; Durand, P.; Bolle, P.A.; Dion, C.; Portetelle,
        D.; Hilger, F.
JOURNAL Yeast (1994) 10:11657-11662
TITLE Sequence analysis of a 40-kb DNA fragment located near the
        left telomere of yeast chromosome X.
        S50769
        #accession
        #molecule_type DNA
        #residues 1-581 ##label VAN
        #cross-references EMBL:Z34098
        #note the nucleotide sequence was submitted to the EMBL Data
        Library, June 1994
        #note neither amino acid nor nucleotide sequence is given

```

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REFERENCE      S56835
authors        Vandebroek, M.; Durand, P.; Portetelle, D.; Hilger, F.
submission    submitted to the Protein Sequence Database, September 1995
accession     S57006
#molecule-type DNA
#residues      1-581 #!label VAW
#cross-references EMBL:Z49491
GENETICS

```

* map position 10L
CLASSIFICATION superfamily alpha-glucosidase
SUMMARY length 581 molecular-weight 67556 checksum 9588

Query	Match	9.9%	Score 100;	DB 4;	Length 581;
	Best Local Similarity	31.5%	Pred. No.	3.70e-01;	
	Matches	17;	Conservative	9;	Mismatches 23;
					Indels 5;
					Gaps 4;
Db	290	gelnnmm-fnfk-htsgenpkckyelipftlkdkflalaesflfientdowstl	341		
		: :	:	:	: :
Qy	92	qplttmmashyqkncppperscatqxif--efsknkd-flvxpfdewpy	142		

RESULT 12 D42402 #type fragment

TITLE cell surface glycoprotein Cb44 variant E - human fragment
ORGANISM *Homo sapiens* #common_name man

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Qy 42 1lnlsrdtaaeexnetveyxsemfdlqep-tclqrtrleykgqlagsitklkgpltmma 98

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Job time : 17 secs.